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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:

April 2, 2000, 21:41:12; Search time 1895.15 Seconds (without alignments) -951.699 Million cell updates/sec

US-08-988-242-1\_COPY (1232\_1825

Perfect score:

Title:

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821193 segs, -- 1518192014 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

1642386 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 1000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	ARO47920 Sequence	Sequence	U24190 Trypanosoma	AL022022 Mycobacte	L27277 Micrococcus	AJ132828 Spermatoz	M30933 E.teneila a	U14400 Equine nerp	AF020275 Homo sapi	AL133030 Homo sapi	X83546 R.norvegicu	AL009198 Mycobacte	APOUCOS HOMO Sapi	APOU0557 Homo sapi	ACOO557 HOMO 6251	AC009516 Homo sapi	AF139019 Cepaea ne	X17207 Chlamydomon	AF087653 Homo sapi	L38713 Gallus gall	M28100 Gallus gall	X95503 M.musculus	SPINOR MININGSCRIPS	ABOO7820 Homo sapi	X12735 Barley Cab-	X68361 M.fascicula	M15764 D.melanogas	M62760 Homo sapien	X61945 D.melanogas	ABO10711 Mus sp. m	M23222 D melanodas	M23221 D.melanogas	Drosophi	003 Drosophi	184 Drosophi	Sequence	38 Simian	5748 Homo	49 Homo s	)1 M.muscu	2 Human IFE	-
SUMMARIES	Ω	AR047920	201	5 TCU24190	MTV023	LURHO	•,		BNII87960						AP000552						CHKPROTAMI	CHKPROTAM	MAZINCEPR	ADOT 8491	AB007820	HVCAB2		DROPENF	Ξ	DMNGZ	ABU10/11	DROFSH					I	HSVGBQ	) AF126748	AF12674		HUMTFEB	DENGMENT
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ALIGNMENTS

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AR047920 3402 bp DNA Sequence 1 from patent US 5820864. AR047920. GI:5970263 RESULT 1
AR047920
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

29-SEP-1999

PAT

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1411

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1471

300

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480

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NOVEL TRYPANOSOMA CRUZI ANTIGEN, AND GENE CODING THEREFOR; THEIR APPLICATION TO THE DETECTION OF CHAGAS' DISEASE PATENT: WO 9605312-A 1 22-FEB-1996; BIO MERIEUX (FR)
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Trypanosoma cruzi Tc40 antigen (Tc40) mRNA, complete cds
U24190
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Trypanosoma cruzi.
Eukaryota; Eudlenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
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Pred. No. 2.1e-116;
0; Mismatches 2;
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1. .3402
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/strainsm="Trypanosoma cruzi"
/strain="G"
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960307
960216.
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                                                                                                                                                                      /db_xref="taxon:5693"
/dev_stage="EPIMASTIGOTE"
818 c 958 9 737
                                                          Other publication CA 2173957
Other publication AU 3169195
Other publication FR 2723589
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99.78;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 3402)
Paranhos-Baccala,G., Lesenechal,M. and Jolivet,M.
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                                           1 (bases 1 to 3402)
Paranhos Baccala,G., Lesenechal,M. and Jolivet,M.
Trypansooms cruzi antigen, gene encoding therefor and detecting and treating chagas disease
Patent: US 5820864-A 1 13-OCT-1998;
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Pred. No. 4.4e-117;
0; Mismatches 0;
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848910.1 GI:2302570
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Lesenechal,M., Franco Da Silveira,J., Mortara,R.A., Duret,L.,
Camargo,M.E., Jolivet,M. and Paranhos-Baccala,G.
Direct Submission
Submitted (06-APR-1995) Mylene Lesenechal, BioMerieux, 22 rue Saint
Jean de Dieu, Lyon 69007, France
Location/Qualifiers
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/protein_de"AaA47657.1"
/db_xref="G1=70646"
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                                                                               Cano, M. I., Mortara, R.A., Jolivet, M.,
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l (bases 1 to 3402)
Lesenechal, M., Duret, L., Cano, M.I., Mortara, R.A., Jolive Canargo, M.E., da Silveira, J.F. and Paranhos-Baccala, G. Cloning and characterization of a gene encoding a novel immunodominant antigen of Trypanosoma cruzi Mol. Biochem. Parasitol. 87 (2), 193-204 (1997)
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/organism="Trypanosoma cruzi"
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1. .35
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1. .3402
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266. 3013
/gene="Tc40"
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Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur. 28 rue du Docteur Roux,
75724 paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:2924430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have Under committee of the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, L., Jagels, R., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, G., Rutter, S., Seeger, K., Skelton, S., Squres, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
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AL022022 AL123456
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540
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                                                                                         1532 CCGCACGTGGGGAGCAAGATCATTGTAATCTAGTGAATCAGCTGGGGATTAATGTCACC
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12,396(6707):190]]
2 (bases 1 to 47852)
Parkhill,J.
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similar to Mycobacterium tuberculosis proteins mtcY19H5.31 (481 aa), MTCI28.11, (515 aa)and MTV051.06. Hydrophobic region atN-terminus. PASTA scores: 297182|MTCY19H5_31 (481 aa) opt:611 z-score: 667.7 E(): 1.1e-29; 32.5% identity in 332aa overlap; and 297050|MTCI28_11 (515 aa) opt: 587 z-score:641.2 E(): 3.3e-28; 30.1% identity in 335 aa overlap. TBparse score is 0.889" ...% identity in /codon_start=1 /transl_table=11 /product**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein Rv3496c"
/product="hypothetical protein Rv3496c"
/db_xref="c1:2924433" 1"
/db_xref="c1:2924433" 1"
/db_xref="c1:2924433" 1"
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FTGAVCLPYTGGAVLPDNGRIDLDRTAPPVEWDEVRGCLTRLAADLSPAAGELG
GPLGAAINQAADTLDGNGDSLHNALRELAQVAGRLGDSRGDIFGTVKNLQVLVDALSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Rv3466c, (MTV023.03c), len: 451. Unknown but similar to Mycobacterium tuberculosis proteins MTC128.12 (530 aa), MTC19H5.30c (508 aa) (MTV051.07). Hydrophobic region at N-terminus. FASTA scores: 297050 MTC128_12 (530 aa) opt:838 z-score: 711.0 E(): 4.3e-32; 35.1% identity in 473 aaoverlap; and 2971821MTCY19H5_30 (508 aa) opt: 821 z-score:697.0 E(): 2.6e-31; 35.1% identity in 453 aa overlap.TBparse score is 0.891"
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NDRAQTLSDOSENIEQVLHVAGPGIRTRYNINDSPAGGTLGGLLSIPNRADVQFTCGG
SPDTAAGPSAPDY TRAREICRERLGPVLRRLTVNYPPIMFHPLNTITAXKGQIIYDTP
ATEAKSETPVPELTWVPAGGGAPVGNPADLQSLLVPPAPGPAPPAPGAGPGEHGGG
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LINVETQALHDATPQVRGAVDGLTSLSRALNRRDEALGGLLAHAKSVTSVLSERAEQVN
KLVBDGNQLFAALDARRAALSALISGIDDVAAQISGFVADNRREFGPALSKLNLVLAN
LNBRRDYITBALKREPATALGEVVGSGPGFNVNVYSVLPGPLVATVFDLVFQPGKL
PDSLADYLRGFIQERWIIRPKSP"
complement [5272. . 6324)
           KDLYSIVKALNDDRKDFVTSLQLLLTFPFPNFGIKQAVRGDYLNVFTTFDLTLRRIGE
                                                                                                                                                                                                                              /note="PS00013 Prokaryotic membrane lipoprotein lipid
                                                   TFFTTAYFDPNMAHMDEILNPPDFLIGELANLSGQAADPFKIPPGTASGQ
complement(2798. .2830)
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/protein_id="CAA17734.1"
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Apone-"RX3496C"
/note-"possible RBS for RY3495c"
complement(4209. .5282)
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complement(2857. .4212)
/gene="Rv3496c"
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complement(4209. 5282)
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/gene="Rv3496c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="R03494c, (MTV023.01c), len: 564. Unknown Pro-rich protein similar to several Mycobacterium tuberculosis proteins e.g. MTC12814.4 (515 aa), MTC129145.28c (516 aa) and (MTV031.09). Has hydrophobic stretch, possibly signal peptide at N-terminus. FASTA scores: 297050|MTC128_14 (515 aa) opt: 1006 z-score: 582.8 E(): 5.9e-25; 34.3% identity in 559 aa overlap: 297182|MTCX19H5_28 (516 aa) opt: 979 z-score:567.7 E(): 4.1e-24: 33.5% identity in 555 aa overlap: 20078244; identity in 555 aa overlap: 29708041; identity in 5508041; identity in 5508044; identity in 5508044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codoi_start=1
//transl_table=11
//transl_table=11
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/protein_id="Ca1.2924431"
/db_xref="G1.2924431"
/db_xref="G1.292431"
/db_xref="G1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis proteins MTC128.13 (390 aa) and MTC119H5.29 (402 aa) and (MTV051.08). Probably
Ilpoprotein, contains possible signal sequence and appropriately possitioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site. FASTA scores: 9p1297050|MTC128_13 (390 aa) opt:553 z-score: 762.1 E(): 0: 33.68 identity in 363 aa overlap; and 297182|MTCY19H5_29 (402 aa) opt: 572 z-score: 667.9 E(): 1.1e-29; 21.88 identity in 362 aa overlap. TBparse
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TVERADVATLPONSYWYDDYTYGSYAGIVAYORPDGSFYAAVKLDLDCKNVLLPANAY
AKVGGTSLLGSLHVELAPPTDRPPTGRLYDGSRITTANTDRPFTEEVFSALGVVVNK
GNVGALEEIIDETHAPARGAGFVNLYPRIABLTAGINROYHDIIDALDGLARVSAL
LARDKDNLGRALDTLPDAVRVLNQNRDHIVDAFAALKRLTMYTSHVLAETKVDFGEDL
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VGVIYHKSIEQLLVVFPALFAAIITSAGGVPQDEGAKLDFKIDLHDPPPCWTGFLPPP
LVRSPADESVREIPRDMYCKTAQNDPSTVRGARNYPCQEFPGKRAPTVQLCRDPRGYV
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PAPHQPAQPAPPPNDNGPPPFTSWMPPGYPPEPPQVPYPATIPPPPPFEGTGPPPGP
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COMPLEMENT(1.1695)
Complement(1.1695)
/gene="Rv3494c"
<1.4780
/note="fragment designated v023. Does not represent a
physical clone"
ite sequence (optimally 5-13bp before the initiation
If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Mycobacterium tuberculosis"
/strain-"H37Rv"
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/note="possible RBS for Rv3494c"
complement(1706. .2860)
complement(1706. .2860)
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/db_xref="G1:2924432"
/db_xref="SPTREMBL:053540"
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/clone="Y13E12"
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/note="Prof.
                                                                                                                                                         Location/Qualifiers
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/product="lprn"
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Nowatzke, W.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                       32802 GCGGCACCGGCGGCACCGGCGCCACCGGCGCCTCGGCGACCCCCGGGTCGGCGGATCCG 32861
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                                                                                                                                                                                                                                                                                                                                        298 GAGCCGCACGTGGGGAGCAAGATCATTGCTAATCTAGTGAATCAGCTGGGGATTAATGTC 357
                                                                                                                                                                                                                                                                                                                                                                                                   358 ACCCAAAGGAGGGTCGTCAGCACTGGAGCGCCGGCCACGACGAGGTCTACGGCGGTGACG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGGATTGGTGGCAGCTAATAGTGGTGCCAGCGCGGCCTCGTCTCCCACAGCCGCGGCG 537
                                                                                                                                                                                                                     178 ACTGACGCGGCGAGTAGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCA 237
                                                                                                                                                                                                                                                                                418 TCCACGACTACCGCCCCCCCAGCGAACAAGTCCATACGGGCACAATGGCCGACCTGTGACG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-FEB-1994) John P. Richardson, Chemistry, Indiana University, Bloomington, IN 47405, USA 4 (bases 1 to 2402)
                                                                                                                                                          Gaps
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Micrococcus luteus Rho factor (rho) gene, complete cds.
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Actinomycetales; Micrococcineae; Micrococcaceae; Micrococcus.
1 (bases 905 to 2402)
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                                                                                                   Score 45; DB 1; Length 47852;
                                                                                                                              0; Mismatches 255; Indels
       /transl_table=11
/product="hypothetical protein Rv3498c"
/protein_id="CAA17735.1"
/db_xref="G1:292443s"
/db_xref="SPTREMBL:053543"
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homology to the Escherichia coli rho gene
J. Bacteriol. 176 (16), 5033-5043 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 AAACCAACAGGAGAAGAAAAGGCCTCCGCGGCA 570
                                                                                                                Pred. No.
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Richardson, J.P.
Direct Submission
                                                                                                7.68;
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L27277.1
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GRRRAGDDDAQOGODRRSDGAOGEDGADADRRGDREDRDDNGRENGRGRNGRNGRDRD
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LAIEBRAKRIVEMGRDVYVLLDSMTRLGRAYNILAPASGGTLSASALYPRKFFG
AARNIENGSSLTILATALVETGSRADEVIFEEFKGTGNWEIRLSRLSRHLAERRIFPAVDV
NASGTRREEALLSQEEVKIMWKLRRVLSGLEQQQALDLLTNKIKDTASNAEFLMLVSK
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NRRNRNERGRRRRGRGGPEVDETELTEDDVLQPVAGILDVLDNYAFVRTSGYLPGPND
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EHPQRVEFGKLVPLYPQERLRLETDPKLIGPRVIDLVSPIGKGQRGLIVSPPRAGKTM
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VTAISDHQRGSSVADRDAAERAAQAPAAPAAETAPAAASSEDAAPAAERPARRRSRRA
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1 (bases 1 to 2028)
Lechtreck, K.F., Teltenkoetter, A. and Grunow, A.
Lechtreck, K.F., Teltenkoetter, A. and Grunow, A.
A 210-kDa protein is Located in a membrane-microtubule-linker at the distal end of mature and nascent basal bodies
Direct Submission
Submitted (07-NOV-1996) William L. Nowatzke, Chemistry, Indiana
University, Bloomington, IN 47405, USA
On Nov 12, 1996 this sequence version replaced gi:968908.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 AGCGIGGICACCACTGGAGCGCCGGCCACGACGAGGICTACGGCGGTGACGICCACGACT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Spermatozopsis similis mRNA for p210 protein, partial.
AJ132828
                                                                                                                                                                                                                                                                                                                                                                                      /function="transcription termination factor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4%; Score 44; DB 1; Length 2402; 49.6%; Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 GGAGAAGAAAAGGCCJTGGGGGCATGTGAAACGAGCTCCGTGGGGATA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 115; Indels

    .2402
    /organism="Micrococcus luteus"

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/db_xref="GI:1666540"
                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="Rho factor"
                                                                                                                                                                                                                                      /db_xref="taxon:1270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
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Spermatozopsis similis
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                                                                                                                                                                                                                                                                                      /gene="rho"
288. .2363
                                                                                                                                                                                                           /strain="EM"
                                                                                                                                                                                                                                                                                                                             288. .2363
/qene="rho"
                                                                                                                                                                                                                                                                 .2363
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947 c
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Matches 113; Conservative
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RQVAYGGECIYPLVLLATTNPQYDLDYTSSGEFDMIGMAEVDLSDWFVNPKREDWYSR
DVELSPHESAAAGYPSGYVYVYLRARGALAALRRACGEGR"
1 808 C 1777 g 189 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   828 CGCGAACTGCGGCGCGCGCGCTGCTGCGGCGCAAACTGCGGCGCCGGCGCCTGGGGGGC 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 649
Unpublished
2 (bases 1 to 2028)
Lechtreck, K.F.
Direct Submission
Submitted (17-FEB-1999) Lechtreck K.F., Botany, University of Cologne, Gyrhofstr. 15, D-50931 Cologne, GERMANY
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTAGTGGCGACGGCGAAACCGGGGTGTGTGTCCTCGGGCACTGACGCGGGGGAGTAGCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 GICATACCAATACGACTICIGCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               768 cececcrececceccececanocceccecrecrerrececcrecrecrececceccecce 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 GGCGCCTGCGGCGCGCGCGCAACTGCGGCGCCGCCGGCTGCTGCTGCGGGCTGCGG 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 ATAGTGGTGCCAGCGCGCCTCGTCTCCCACAGCCGCGGAAACCAACAGGAGAAAA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AGATCATTGCTAATCTAGTGAATCAGCTGGGGATTAATGTCACCCAAAGGAGCGTCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 GCACTGGAGCGCCGGCCACGACGAGGTCTACGGCGGTGACGTCCACGACTACCGCCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                708 GAACTGGGGCGCAAGCGCCTGCTGCTGCGGCGCCCGGCGCGGACTGAGGCTGCGGCGC
                                                                                                                                                                                        /function="putative microtubule-membrane-linker"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIMMAX 767 bp mRNA INV
E.tenella antigen LPMC61 mRNA, partial cds.
M30933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6;
0; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43.2; DB 7;
Pred. No. 6;
                                                                                                                                                                                                                      /product="p210 protein"
/protein_id="CAB40552.1"
/db_xref="GI:4584086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           557 AGGCCTCCGCGG 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                               source
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ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
              JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                            AUTHORS
                                                                           JOURNAL
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                                                                                                            FEATURES
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/protein_id="AAA29079.1"
/db_xref="G1:158896"
/translation="LRLLLKLLLLLGQQKHWPERQQQQPQPWLDRQQQQQHNQQL
                                              E.tenella (strain Wisconsin), mRNA to cDNA.
Eimeria tenella
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                 Draft entry and computer-readable sequence for [Unpublished (1990) Synergen, INC., 1885 33rd St., Boulder,CO 80301] kindly submitted by C.S.Ko 12-DEC-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 gene homologue
                                                                                                                                                                    Ko.C., Smith.C.K.II. and McDonell,M.
Identification and characterization of a target antigen of a monoclonal antibody directed against Elmerla tenella merozcites Mol. Biochem. Parasitol. 41, 53-64 ((1990))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 GCTCAGGCCACTGCTGCTGCTGTTGCTCTGGCCACAGCTGCTGCCGCTGGCCCTCAGGCC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 GCGACGGCGAAACCGGGGTGTGTGTCCTCGGGCACTGACGCGGCGAGTAGCAGTCATACC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Equine herpesvirus 4 (EHV4) genome, thymidine kinase (TK) and 91ycoprotein H (9H) genes.
91ycoprotein H (9H) genes.
91ydoprotein H (9H) genes.
91ydoprotein H (9H) genes.
91ydoprotein; thymidine kinase.
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The nucleotide sequence of the equine herpesvirus 4 thymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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240 c 249 g 77 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.8; DB Pred. No. 7.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Eimeria tenella"
/db_xref="taxon:5802"
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/note="antigen LPCM61"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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M30933.1 GI:158895
                                                                                                                                                 (bases 1 to 767)
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TITLE
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
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TITLE
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KEYWORDS
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                       KEYWORDS
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HSE4
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                                                    SOURCE
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VITRTAPNIGLTYSLDGVNIAKPIVISYITYGNCQVSRATIRSVYLDHPGHTQSCVYC
GSVFMRYMASGAIMDLIYIDDKDVELQLVAGENSTIPAFNPKLYTPSMNALLMFPNGT
VTLMSAFASYSAFKIPSTYLWASIGGLLLAILILYVIVKMLCGGVINNDYSLLLNSE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /proteIn_id="BaA03380.1"
/db_xrsf="G1:221824"
/db_xrsfiion="NVSLIAFDNLDLSRKGAYYLYYLLSERLKRGGVPVHVNRA"
/ 1377 c 1499 g 1545 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Massa, S.M. and Longo, F.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 2479)
Zhang,C., Zhang,J.S., Martignetti,J.A., Massa,S.M. and Longo,F.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5073 GCGGCGGCGAGGCCTGCTGCGGCGGCGGCGAGGCTGCTGCGGCGGCGGCGAGGCCTGCT 5132
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Rattus norvegicus leukocyte common antigen receptor (LAR) gene,
trans-spliced alternative untranslated exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4953 GCGAGGGCTGCGGCGGCGGCGGGCTGCGGCGGCGGCGGCGAGGGCTGCGGCGGCG 5012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 GCGACGGCGAAACCGGGGTGTGTGTCCTCGGGCACTGACGCGGCGAGTAGCAGTCATACC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCCGCGCCTCCTGCCGCGCGCGCGATCGGCTGAGCCGCACGTGGGGGAGCAAGATCATT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 2479) Stango, 2, Zhango, 2, Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5013 GCGGCGAGGGCTGCGGCGGCGGCGAGGCCTGCTGCGGCGGCGGCGAGGGCTGCTGCG
                                                                                                  4777. 4782

//note="put. polyadenylation signal(gH); putative"

4893. 5315

5395. 5403

//note="mut. replication origin; putative"

//note="put. replication origin; putative"

//note="put. replication origin; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 GCGCCGGCCACGACGAGGTCTACGGCGGTGACGTCCACGACTACCGCCCCGCAGCGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 AGTCCATACGGGCACAATGGCCGACCTGTGACGGCTGGATTGGTGGCAGCTAATAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                    complement(5755. .>5880)
/note="putative; ORF4 (UL21 homologue)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41.6; DB 16;
Pred. No. 12;
0; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5253 GCGAGGCTGCTGCGGCGGCGCGAGGCCTGC 5284
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                                                                                                                                                                                                                                                                                                                                                                    complement (5755
                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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Best Local Similarity 44.1%;
Matches 173; Conservative
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U87960.1 GI:1857717
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Rattus norvegicus
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APLESELVPRETLKTAMGVSLAFEVNLGQRRPDCVGTVQFGHGSDAKGVCILIELKTC
FSKNNNTASKNLQKRGGMRQLHDSCKTLPAFVLFPPGSGELILAPPLIVFYAPRGMRYLR
VTRLSPQVYVSONAAVLSGTIGRLABYSPPIGERSTRRKCYFRTNGKAFRAKTTGSI
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MASAASGGSPTLYFPEPMAYWRTLFETDVISGIYDTQNRKQQGNLAVDDAALITAHYQ
SRFTTPYLILHDHTCTLFGGNSLQRGTQPDLTLVFDRHPVASTVCFPAARYLLGDMSM
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VNTCHFLRSGRVWRDGWGELPTSCGAYKHRATOMDAFOERVSPELGDTLFALFKTOEL
LDDRGVILEVHAWALDALMLKLRNLNVFSADLSGTPRQCAAVVESLLPLMSSTLSDFD
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WYHNNTRNVTRYDRITMEPVYNNNLSSTTFFVAISERNFRTVNTPLGASVFWILKSAL
NPPKHQPCIANVPEPGDPRGPCVNSTVSLFFNDNLEPFLMTKNLLEFEVLPDNYITGW
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TKTLTYISPFAAVWPITAFHAGITVMGCDTTQAIAYLGNGFMGLQISSVNNPPLEMIV
APNDVRARIVNRLPPRRRLEPPGPYAGPITKVYVLSDGNFYLGHGMSKISREVAAYPE
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IENELRKPMYEHRSLLKSVYAYSRKPLPNAVSFANRLITAMYKEAIKDRITWNSTMRE
VLFFAVGAAAGSHVILTDGPDLGLHAHKDSSMFLSLNRNILLLCTAMCTASHAVSAGV
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EDDGTTIHSYGRSANGILNSRIAYNFDAVRVFTPELASCSTKLPKVLVVLPLASNRSY
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complement(99 .104)
/note="put. polyadenylation signal (UL24); putative"
/note="put. polyadenylation signal (UL24); putative"
complement(115 .120)
/note="put. polyadenylation signal (UL24); putative"
/note="put. polyadenylation signal (UL24); putative"
/note="putative; ORFI (UL24 homologue)"
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/partial
/note="08ff2; (TK)" /codon_start=1
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2049. .2054
7. note="put. polyadenylation signal (TK); putative"
7.2127. .2133
/note="putative"
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Dept. Veterinary Pathology. University of Glasgow
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/note="put. TATA box (TK); putative"
kinase gene
J. Gen. Virol. 71 (Pt 8), 1801-1805 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Equine herpesvirus 4"
                                                                                                                                                                                                                                                           Dept. Veterinary Pathology. University of
Vet School
Bearsden Roda, Glasgow G61 1QH. Scotland
UK.
                                                                                                                                                               Unpublished (1993)
Submitted (10-SEP-1990) to DDBJ by:
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/db_xref="GI:221822"
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/db_xref="GI:221821"
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/db_xref="G1:221823"
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/note="putative"
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/note="region of cag expansion"
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/note="similar to NotI jumping clone sequence with GenBank

Accession Number X95831"

127. .285
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Submitted (30-JAN-1997) Neurology, Veterans Administration Medical
Center at UC San Francisco, Neurology (127) 4150 Clement St., San
Francisco, CA 94121, USA
Location/Qualifiers
1. 2479
//Organism="Rattus norvegicus"
//db_xref="taxon:10116"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
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/product="leukocyte common antigen receptor"
2457, .2479
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Koob,M.D., Benzow,K.A., Moseley,M.L. and Ranum,L.P.W.
Direct Submission
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Homo sapiens expanded SCA7 CAG repeat.
AF020275
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/chromosome="3"
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/rpt_type=tandem
/rpt_unit=CAG
1650. 2/15
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Best Local Similarity 57.9%;
Matches 73; Conservative (
                                                                                                                      /gene="LAR"
1. .2479
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/gene="LAR"
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Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.blochem.mpg.de/proj/cDNA/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOWLNYRDLORLORESOREVLRLOROLMLOQGNGGAWPEAGGOSATCEEVRROMLALE
RELDORRRECOELGAQAAPARRRGEEAETOLOAALLKNAWLAEENGRLGAKTDWVRKV
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EIQALQCRPGHPPEQPWETSQMPESQVKGSRRPKFHARPEDYAVSQPNRDIQEKREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"hypothetical protein"
/protein_id-"CAB61382.1"
/db_xref="G183432"
/tb_xref="G183432"
/translation-"SEQASAPLAKDKQIEELRQECHLLQARVASGPCSCLHTGRGGPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEESPVALGESASVPQVSETVPASQPLSKKTSSQSNSSSEGSMWATVPSSPTLDRDTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DKFZp434H177"
/note="similarity to peripheral benzodiazepine receptor
interactingprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .3932/

/organism="Homo sapiens"

/db_xref="raxon:0606"

/clone="DKFZp434H177"

/clone="lib="434 (synonym: htes3). Vector pSportl; host

/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSM801297 3932 bp mRNA PRI 17-NOV-1999
Homo sapiens mRNA; cDNA DKFZp434H177 (from clone DKF2p434H177).
AL133030
                                                                                                                                                                                                                                                                                                      145 GCGACGGCGAAACCGGGGGTGTGTGTCCTCGGGCACTGACGCGGCGAGTAGCAGTCATACC 204
                                                                                                                                                                                                                                                                              334 GIGGCGCCGCTGCCGCTGCCTGCCGCTGCGGAGGCGGCGGCGCTGCTGCT
                                                                                                                                                   ö
                                                                                                  Score 40.4; DB 11; Length 477; Pred. No. 26;
                                                                                                                                                   Indels
                                                                                                                                                 71;
                                                                                                                                                                                                                                                                                                                                                                265 GCAGCCGCGCCTCCTGCCGCGCGCGCGATCGGCTG 298
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                      42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="DKFZp434H177"
                    þ
/rpt_unit=cag
164 c 172
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                                                                                                    Query Match
Best Local Similarity 53.9%;
Matches 83; Conservative
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VPLTWOKYS VRIMSLICCESLIDSON OF THE TOTAL TRANSPARATED THE TOTAL OF THE
SEVDDLEPDSVSLALEWGGSAAPAAPKLKIFNAQYNYNPFEGPNDHPEGELPLTAGDY
IYIFGDMDEDGFYEGELEDGRRGLVPSNFVEQIPDSYIPGCLPAKSPDLGPSQLPAGD
IAZIFGDMDEDGFYEGELEDGRRGLVPSNFVEQIPDSYIPGCLPAKSPDLGPSQLPAGG
BALEBDSLLSGKAGGVVDRGLCQMVRVGSKFEVATEILDTKTEACQLGLLQSNGKOG
LSRPLLGTKGVLRMAPMQLHLQNVTTNTWVYSSHRPHVYYLDDREHALTPAGV
SCYTFOGLCPGTHYRAVEVRLPRDLLQVYMGTMSSYVTFDTLLAGPPYPPLDYLVER
HASPGYLVVSWLPVTIDSAGSSNGVQVTGYAVYADGLKVCEVADATAGSTLLEFSOLO
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1 (bases 1 to 3941)
2 hang, J.S. and Longo, F.M.
3 preferential Loneryous system, coordinated with cell growth and generates novel isoforms containing extensive CAG repeats
3 Cell Biol. (1995) In press
2 (bases 1 to 3941)
2 hang, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-DEC-1994) J.S. Zhang, Univ. of California San Fransisco, Neurology, 4150 Clement Street, Building 1 Room 219H, San Francisco CA 94121, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X83546.1 GI:673488 cell adhesion molecule; leucocyte common antigen-related protein nerve growth factor; trinucleotide repeat; tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R. NOTOWERS SOLUTION TO THE SOLUTION SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 CAAGGCAGCCGCGCCTCCTGCCGCGCGCGATC-GGCTGAGCCGCACGTGGGGGAGCAAGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 3932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .3941
/organism="Rattus norvegicus"
/strain="Sprague-dawley"
/db_xref="taxon:10116"
/clone="pRLAR4.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 40.4; Di
Best Local Similarity 52.9%; Pred. No. 22;
Matches 109; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 TCATTGCTAATCTAGTGAATCAGCTG 345
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Rattus norvegicus
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SRVLITSIDGVPGSDYINANYIDGYRKONAYIATGPLPETMGDFWRWYWEGRTATYV
MWTRLEBERSRYKCDGYWPARCTETYGLIOYTLYDTVBLATYTWRIFELHIKSGSSERRE
LMQFGFWAWPDHGDFYTPTLAFLRRYKACNPLDAGPWYHGSAGVGRTGCFIVIDA
MLERMKHEKTVDIYGHVTCMRSGRNYWVQTBDOYVFIHEALLEAAMCGHTEVLARNLY
AHIQKLGQYPPGESYTAMELEFKLLANSKAHTSRFISANLGYRKRLYNINYYELT
RYCLQPPRGSSYTAMELEFKLLANSKAHTSRFISANLGYRKRLYNINYYELT
RYCLQPPRGSSYTAMELEFKLLANGYRHYRKTANTURFLYNINYYELT
INTKLREMGREKCHGYNINASFLOGYROKAYINTON
                                                                                                                                                                                                              /translation="SIGLKDSLLAHSSDPVEMRRLNYQTPGSSAPSCPNISSMRDHPP
IPITDLADNIERLKANDGLKFSQEYESIDPGQQFTWENSNSEVNKPKNRYANVIAYDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQFQFTDWPEQGVPKTGEGFIDFIGQVHKTKEQFGQDGPITVHCSAGVGRTGVFITLS
IVLERMRYEGVVDMFQTVKTLRTQRPAMVQTEDQYQLCYRAALEYLGSFDHYAT"
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Tobases 1 to 69350)

Hartis, D., Gordon, S.V., Esjameier, K., Gas.S., Barry III, C.E.,

Hartis, D., Gordon, S.V., Esjameier, K., Gas.S., Barry III, C.E.,

Tekata, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,

Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S.,

Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,

Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,

Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,

Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTV004 69350 bp DNA BCT 18-JUN-1998
Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.
AL009198 AL123456
AL009198.1 GI:3242262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="brain"
/clone_lib="cDNA library (custom made by Strategene)"
<1. .1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 CGGCCACTGACGCGCGAGTAGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                               common antigen-related protein"
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Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
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/note="alternate spliced 3'UTR with CAG repeats"
1 1069 c 1061 g 810 t
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erratum:[[published erratum appears in Nature 1998 Nov 12:396(6707):190]]
2 (bases 1 to 69350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 6.8%; Score 40.4; DB 12; Best Local Similarity 56.9%; Pred. No. 22; Matches 74; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="insertion sequence LASEa"
                                                                                                            /product="leucocyte common
/protein_id="CAA58537.1"
/db_xref="G1:693993"
/db_xref="SPTREMBL:Q63296"
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Nature 393 (6685), 537-544 (1998)
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                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                 available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparese (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream initiation codon.
                                                                                                 tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 20, 1998 this sequence version replaced 91:2661623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Rv3346c, (MTV004.02c), len: 85, unknown, similar tow. leprae hypothetical protein TR:E332951 (EMBL:298271) MLCB1779.16c (91 aa), fasta scores; opt: 349 z-score: 070.13 E(): 6.6e-32, 67.4% identity in 95 aa overlap. Also highly similar to upstream ORF Rv3355c (MTV004.12c) (85.6% identityin 97 aa overlap).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="hypothetical protein Rv3346c"
/protein_id="CAALS731.1"
/db_xref="GI:S61625"
/db_xref="SPTREMBL:050377"
/translation="MTVRAVLRRTVGAQWPILAGVNFWRRGALLIGIGVGVAAVLRLV
Parkhill,J.

Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium Submitted (11-JUN-1998)
                                                                                                                                                                                                                                                                Notes: Details of M. tuberculosis sequencing at the Sanger Centre are
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//note="fragment designated v004. Does not represent
physical clone"</pre>
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1. .69350
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
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/db_xref="G1:2661626"
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complement(144. .401)
/gene="Rv3346c"
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/note="direct repeat 2"
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/note="direct repeat 3"
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/gene="Rv3346c"
144. .350
/gene="Rv3346c"
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POGYPRAYOS GENERAL MORACE TO A REAL SOFT THE SOLVE OF LINE OF PROGPRAYOS GENERAL MORACE AND CONTROL MORACE A
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ITISPITLPPAQNRWTFPVGPFFGLGVVNISGIETKDLAGRWTLQLGNLNIDTRING
SPYTVNWSTPAVTIFPNGISIPNNHALLASASIGTLGFTIPGFTIPARAPLENTIDI
DQQUDGFSTPPITIDRIPLNLGANTPUGHTINGVNIPATPGFGWTTAPSGGFG
DGGVSGFGNFGSSGWWNQAQTEVAGGSGFANFGSLGSGVLNFGSGCVSGLYNTGGL
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NFGVFNSGSYNTGVGNAGTASTGLFNVGGFNTGVANVGSYNTGSFNAGNTNTGGFNPG
NVNTGWLNTGNTNTGIANSGNVNTGAFISGNFSNGVLWRGDYEGLWGLSGGSTIPAIP
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IGLGNAGSGNVGWANMCLGNIGFGNTGTNNLGIGLTGDNQSGIGGLNSGTGNIGLFNS
GTGNIGFFNSGTANFGLFNSGSYNTGIGNSGVASTGLVNAGGFNTGVANAGSYNTGSF
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SIHLGIDPTFDVGPITVDPITLTIPGLSLDAAVSEIRMTSGSSSGFKVRPSFSFFAVG
PDGMPGGEVSILQPFTVAPINLNPTTLHFPGFTIPTGPIHIGLPLSLTIPGGT
ATVDPAAVAVNRMAMRALAMSNLLGQNAAA IAAVEAEY ELMWAADVAAMAGY HSGASA
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TAPSSGFFNTGGGGGSGFSNSGSGMSGVLNAISDPLLGSASGFANFGTQLSGILNRGA
GISGVYNTGTLGLVTSAFVSGFMNVGQQLSGLLFAGTGP"
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gene from: 76 to: 1582" complement(10139. .10143)
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/gene="PPE"
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/note-"possible RBS upstream of Rv3347c" complement(10277. .11310) /gene-"ppE" /note-"Identical to MTCY1A6 from: 23082 to: 24115"

/gene="PPE

/note="IS1608'" 10711. 11202 /gene="Rv3348"

/0711. .11202 /gene="Rv3348" 10711. .11199 /gene="Rv3348"

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/rpt_family="MIR"
/evidence-not_experimental
complement(8880..9173)
/rpt_family="Aluy"
/evidence-not_experimental
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/rpc_family="(TAAA)n"
/evidence-not_experimental
complement(4122. .4305)
/rpt_family="Alusg/x"
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/rpt_family="MER31B"
/evidence=not_experimental
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/evidence=not_experimental
complement(1717. 2021)
/rpt_family="AluSx"
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'evidence=not_experimental
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complement(11968..12299)
/rpt_family="AluJo"
/evidence=not_experimental
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complement(16477. 16655)
/rpt_family-"Alusc"
/evidence-not_experimental
                                                                                                                                                                                                                                                                              complement(1. .667)
/rpt_family="L1M4c"
/evidence=not_experimental
complement(1010. .1716)
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17597. .17671
                                                                                                1. .149618
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t_family="L1M4c"
      with 69793-bp overlapping.
Sequence updated (26-Oct-1999).
Location/Qualifiers
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                                                                                                         source
                                                                       FEATURES
/note="Rv3348, (MTV004.04), len: 163 aa; unknown, identical to M. tuberculosis hypothetical protein TR:996334 (EMBL:89864) MTVOIA6.25 (163 aa). Partially similar to several insertion elements, e.g. Partially P19834 [VIII_STRCI INSERTION ELEMENTIS116, (399 aa, 28.5% identity in 15% aa overlap)."
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//trans_table=11
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GKSKSDVIDAEVLTRASEVFDLTPLTLPTPAQLALRRSVIRRAGAVIDANRSWRRLMS
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Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Blology: 35 Shimanomachi, Shinjuku-ku, Tokyo 160-0016, Japan (E-mail:nshimizuedmb.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370, On Oct 29, 1999 this sequence version replaced gi:6006352.
This is a complete sequence of the insert of KBI172D5 clone. The proximal adjacent clone is KBI183D5 (Acc.#AP000552) with 67422-bp overlapping. The distal adjacent clone is KBI323B2 (Acc.#AP000557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Rv349c, (MTV004.05c), len: 246 probable transposase pseudogene fragment, similar to part of TR:050911 (EMBL:U10634) IS204 PUTATIVE TRANSPOSASE from NOCARDIA ASTEROIDES (377 aa), fasta scores; opt: 288 z-score: 322.6 E(): 8.3e-11, 48.5% identity in 97 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 37084 GCCAGCACGCCAACTCCGGCAATGGCGGTGGCGGCGGTACCGGCGGGGGCACCC 37143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37024 GCGCCGACGCCGTGACGGGGGCATGCCGGCACCGGTGGACGTGGCGGGTTACTGGCCG 37083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 ACCAATACGACTICTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCAGCGCCAGCC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 GTGGGACGACGAAACCGGGGTGTGTCTCGGGCACTGACGCGGGGAGAGCAGTCAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Homo sapiens genomic DNA, chromosome 22q11.2, BCRL2 region,
clone:KB1172D5.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA sequence from clone KB1172D5 on chromosome 22q11.2 published Only in DataBase (1999) In press 2 (bases 1 to 149618) Shimizu.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 69350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 AAGGCAGCCGCGCTCCTGCCGGGGGGGGATCGGCTGAGCCG 303
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Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Rv3349c"
complement(11239. .11979)
/gene="Rv3349c"
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AP000556.2 GI:6139049
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Shimizu, N.
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Best Local Similarity 53.1%;
Matches 86; Conservative (
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AP000556/c
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rpt_fam cwidenc cmyldenc rpt_fam cwidenc 7832 rpt_fam evidenc 1993 rpt_fam rpt_fam cvidenc 2304.	2288823013 /rpt_family"Aluxb8" /evidence=not_experimental 2301423323 /rpt_family"Alux" /evidence=not_experimental 2332423496 /rpt_family"AluxB8" /rpt_family"Aluxb8" /rpt_family"Aluxb8" /evidence=not_experimental complement(2409824406) /rpt_family"Aluxb8 /evidence=not_experimental		/evidence=not_experimental complement(2634026623) /rpt_family=Nalusx /evidence=not_experimental 2673126833 /rpt_family=1.27 /evidence=not_experimental complement(2679826898) /rpt_family=1.27 /evidence=not_experimental 2689927029 /rpt_family=FLAM_C* /evidence=not_experimental 2689927039 /rpt_family=FLAM_C* /rpt_family=FLAM_C* /evidence=not_experimental complement(2703727337) /rpt_family=Alux* /evidence=not_experimental complement(2703727337)	# 10
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repeat. repeat. repeat. repeat. repeat. repeat.	Query Matches  Qy 141  Qy 201  Qy 261  Qy 261  Db 35611  Qy 320  Qy 320	RESULT 15 AP000557 LOCUS DEFINITION ACCESSION VEXTON KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL TITLE

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keio.ac.jp, Tel:81-3-3351-2370, nce version replaced gi:6006353. ce of the insert of KB132B2 clone. The S KB1172D5 (Acc.#AP000556) with 69794-bp	nt clone is KB1802C5 (Acc.#AP000558)						in a T	ental		ental	nta]		ental		ental	,	3)	ental		ental		ental	ental	(2)	ental	ental		ental 5)	a to		ental		enca. 478)	ental	nrtal	} (266
(E-mail:nshimizu@dmb.med.keio.ac.jp, Fax:81-3-3351-2370) On Nov 2, 1999 this sequence version This is a complete sequence of the in proximal adjacent clone is KBI172D5	overlapping. The distal adjacer with 21623-bp overlapping. Sequence updated (29-Oct-1999).	Location/Qualifiers 1150036	/organism="Homo sapiens' /db_xref="taxon:9606"	/chromosome="22" /clone="KB1323B2"	/map="22q11.2" 519594	/rpt_family="(TTTG)n"	complement(554565)	/rpt_ramily="FLAM_C" /evidence=not_experimental	566594 /rpt_family="(TTTG)n"	/evidence=not_experimental	/rpt_family="FLAM_C"	8131106 /rot familitalings"	/rpc_ramiir	/rpt_family="AluJb"	/evidence=not_experimental 26132915	/rpt_family="AluSp"	complement(3253, .3353)	/rpt_tamily="L1ME3A" /evidence=not_experime	complement(33963501	/evidence=not_experime	complement(3//940/2) /rpt_family="AluSq"	/evidence=not_experime 41324429	/rpt_family="AluSx" /evidence=not_experime	<pre>complement(55535635) /rpt_family="MER5A"</pre>	<pre>/evidence=not_experimental complement(59306220)</pre>	/rpt_family="AluY" /evidence=not_experimental	73307497 /rpt_family="MIR"	/evidence=not_experimental complement(97259855)	/rpt_family="LiME3A"	990110191 /xxt fam:11x="%1"xbe"	/ipt_ramily= Aluibo /evidence=not_experimental	/rpt_family="(TG)n"	/evidence=not_experime complement(22321224	/ipc_ramiry nam /evidence=not_experimental 22670 22733	/rpt_family="(TA)n" /evidence=not_experimental	complement(22743229
(E-mail: Fax:81-3 COMMENT On NOV 2 This is proximal	overlapp with 216 Sequence	FEATURES Source		-	repeat region		repeat_region		repeat_region	repeat_region	1	repeat_region		norfar-radar.	repeat_region		repeat_region		repeat_region		repear_region	repeat_region		repeat_region	repeat_region		repeat_region	repeat_region		repeat_region	40000	repear_regroup.	repeat_region	repeat region		repeat_region

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1; 1; Gaps Query Match
6.8%; Score 40.4; DB 10; Length 150036;
Best Local Similarity 52.9%; Pred. No. 17;
Matches 109; Conservative 0; Mismatches 96; Indels 1; 96; Indels

Db 119367 AGCAGCGCCGCCTGCAGTGTCTCGGCCTCCTCGCCACGTCGCCGCCGGGGCCGCC 119426 141 AGTGGCGACGGCGAAACCGGGGTGTGTGTCTCGGGCACTGACGCGGCGAGTAGCAGTCA 200 ò

201 TACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGCCAGC 260 ò

Db 119427 IGCGIGCCCAGCTCCTGGCACCTCGCCCCGCTGGTCCAGCTCCCAGCTCCAGCCCAGC 119486

QY 320 TCATTGCTAATCTAGTGAATCAGCTG 345

9.7

Db 119547 CCGTTGCCCTGCTGAAGCATCAACTG 119572

Search completed: April 2, 2000, 21:42:57 Job time: 10416 sec

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TOPOLOGY:
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Best Local Simi
Matches 594;
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1075.390 Million cell updates/sec
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                                                                                          April 2, 2000, 22:08:30 ; Search time 66.13 Seconds
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*

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7: /cgn2_6/ptodata/1/ina/PCTUS9_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PcTUS9_COMB.seq:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-718-661-1

US-08-042-379C-60

US-08-217-327-3

US-08-298-687A-3

US-08-298-687A-3

US-08-298-687A-3

US-08-298-829-3

US-08-798-829-3

US-08-787-325-2

US-08-788-829-3

US-08-88-93-3

US-08-88-93-3

US-08-88-93-3

US-08-88-93-3

US-08-98-829-25

US-08-130-114-115

US-07-884-811-15

US-07-884-811-15

US-08-194-0888-15

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US-08-469-802B-5
US-08-267-803B-5
US-08-469-802B-2
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594
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Listing first 45 summaries
                                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 1000000
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37.
36.
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APPLICANT: DARANHOS-BACCALA, Glaucia
APPLICANT: LESENECHAL, Mylene
APPLICANT: JOLIVET, Michel
TITLE OF INVENTION: ME THE LATTER: THEIR APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: CHAGAS DISEASE
TITLE OF INVENTION: CHAGAS DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
STREET: 10.Suth Washington Street, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,917
FILING DATE: 07-JUN-1995
CLIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REFERENCE/DOCKET NUMBER: 30,024
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 594; DB 2; L ilarity 100.0%; Pred. No. 7.1e-153; Conservative 0; Mismatches 0:
                     US-08-267-803B-3
US-07-814-210-3
US-07-812-421-3
US-07-661-610C-11
US-08-674-168-24
US-08-146-930-1
US-08-146-930-1
US-08-146-930-1
US-08-146-930-1
US-08-146-930-1
US-08-146-930-1
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US-08-714-677-11
US-08-393-540-11
US-08-714-537-11
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Patent No. 5820864
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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US-08-480-917-1
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1 CAGGTACAGCGTAACGGCTTTTGCTTCAATCGTACAGCCGACGGTAGCTGCGTCCTGGCT

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Sequence

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                                                               137 CGGTAGTGGCGACGCGGAAACCGGGGTGTGTGTCCTCGGGCACTGACGCGGCGAGTAGCA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08042747A
Patent No. 5487969
GENERAL INFORMATION:
APPLICANT: Eberle, Richard
APPLICANT: Scinicariello, Franco
APPLICANT: Scinicariello, Franco
APPLICANT: Hilliak.
ITILE OF INVENTION: Cloning and Amplification of Monkey B
TITLE OF INVENTION: Virus Genes
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cox & Smith Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38.2; DB 1; Length 2 Pred. No. 0.11; 0; Mismatches 123; Indels
   Indels
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COMPUTER: IDAD PO disk
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COMPUTER: IDAD PO COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/042,747A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAYMOND, W. Bradley
REGISTRATION NUMBER: 35186
REFRENCE/DOCKET NUMBER: S-0072.179
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000 DATE:
TELECOMMUNICATI
   68;
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F: 112 East Pecan Street, Suite 2000
San Antonio
   Mismatches
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Best Local Similarity 47.7%;
Matches 112; Conservative (
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nucleic acid
EDNESS: single
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TELEX: 767609
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   Conservative
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US-08-042-747A-7/C
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US-08-042-747A-7
   80;
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tumor suppressor proteins and methods for their isolation
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                                                                                                                         1292 GACATGTCGATTCGATTGACGATCTTCCATCTCCGGTCCTCCCGCAGGGAAGAACAGCAG
                                                                                                                                                                                                                                               GACGCGCGAGTAGCAGTCATACCAATACGACTTCTGCCGCTGCTGCTGCATCCCTGCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCACGTGGGGAGCAAGATCATTGCTAATCTAGTGAATCAGCTGGGGATTAATGTCACC
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Pred. No. 0.059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08718661
Patent No. 5876972
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic
TITLE OF INVENTION: tumor su
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.6%;
54.1%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2790 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2790 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 542..2545
US-08-718-661-1
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Best Local Similarity
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US-08-718-661-1

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329 ATCTAGTGAATCAGCTGGGGATTAATGTCACCCAAAGGAGCGTCGTCAGCACTGGAGCGC 388
                                                                                                                             135 GGAGGACGGGGAAGGAAGAAGGAGGGGGGGGTGCCGCGAGGCCGCATCCCGGGGCGCG
                                                                                                                                                                          389 CGGCCACGACGAGGTCTACGGCGGTGACGTCCACGACTACCGCCCCGCAGCGAAC 443
                                                                                                                                                                                                                            Ouery Match
6.3%; Score 37.6; DB 4; Length 2115;
Best Local Similarity 63.0%; Pred. No. 0.15;
Matches 58; Conservative 0; Mismatches 34; Indels 0
                                                                                                                                                                                                                                                                                                                                       Sequence 60 Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
APPLICANT: Odicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED TITLE OF SEQUENCES: 88
CORRESPONDENCE SADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/POCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPAN: (312) 474-6300
TELEPAN: (312) A74-6300
TELEPAN: (312) A74-6300
TELEPAN: (312) A74-6300
TELEPAN: (312) A74-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 762..2115
US-08-474-379C-60
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517 CIGCCCCCCCCCCCCCCCCCCCCCCCCCAGCCCCCAGCCCCCAGTGTCAGCCGCCGCCGCCG 636
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Pred. No. 0.21;
0; Mismatches 44; Indels
                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: John, Maliyakal E
APPLICANT: John, Maliyakal E
APPLICANT: Barton, Renneth A
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: P.O. Box 2113
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                               STATE: WI
COUNTRY: USA
ZIP: 5370-1313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
                                                       637 CCCCCCTGCCGCCGCCCCCGCGG 668
                                  272 CGCCTCCTGCCGCGCGCGATCGGCTGAGCCG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICALL...
APPLICATION: 435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 112299083:
TELECOMMUNICATION INFORMATION:
"""FPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1122990831
                                                                                                                                                              Sequence 3, Application US/08217327
Patent No. 5474925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .vroLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2%;
Best Local Similarity 58.9%;
Matches 63; Conservative (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coker 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: Coker
TISSUE TYPE: F
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: H6.
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-217-327-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                             RESULT 5
US-08-217-327-3
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Sequence 3, Application US/08298687A
Patent No. 5521078
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gossyptum hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 15 day old fiber cells
TISSUE TYPE: fiber cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FRIDK DAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-6CT-1988
ATTONNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,687A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-2478
TELEFAX: (608) 251-5139
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGHH: 913 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%;
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Best Local Similarity 58.99
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKFB15A1
                                                                                                                                                                                                                                                                                                         Wisconsin
                                                                                                                                                                                                                                                                                   CITY: Madison
STATE: Wiscons
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                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CLONE: H6
US-08-298-687A-3
                                             US-08-298-687A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 TCCACCCAGTICICCICCTCCTGCAACTCCACCACCTGCTTCTCCTCCTCCTGCAACTCC 379
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                        258 AGCCAAGGCAGCCGCGCTCCTGCCGCGGCGCGATCGGCTGAGCCGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: P.O. Box 2113, First Wisconsin Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 15 day old fiber cells
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CKFB15A1
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICTOSOft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,970A
FILING DATE: 19920518
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-1988
ATTORNEY,AGENT THEORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5139
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                Sequence 3, Application US/07885970A Patent No. 5495070 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                    Wisconsin
: USA
                                                                                                                                                                                                                                                                                                                                                CITY: Madison
STATE: Wiscons
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 53701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CLONE: H6
US-07-885-970A-3
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198 TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCAGCGCC 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 ACCICCAGCITCICCACCICCACCACCACCAGCTICICCAC 426
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                APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36.6; DB 1;
Pred. No. 0.21;
0; Mismatches 44;
                                                                                                                                 ADDRESSEE: Nicholas J. Seay, Quarles & Brady STREET: P.O. Box 2113, First Wisconsin Plaza CITY: Madison CATTE: Wisconsin COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELORMENTAL STAGE: 15 day old fiber cells
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRATE COURCE:
CLONE: H6
                                                                                                                                                                                                                                COUNTY: USA
ZID: 53701
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICTOSOft WOOG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,829
FILING DATE: 19-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/298,829
FILING DATE: 19-OCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 11-NOV-1990
PRIOR APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: SCAY, NICHOLAS J.
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5139
INFORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 DASS PAIRS
TYPE: NUCLEIC CAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/08787335
; Patent No. 5981834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Gossypium hirsutum
STRAIN: Coker 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%;
58.9%;
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Best Local Similarity 58.9
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
    GENERAL INFORMATION:
APPLICANT: John,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-787-335-2
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0
         Sequence 2, Application US/08530797
Patent No. 559718
GENERAL INPOMBATION:
APPLICANT: John Wallyakal E.
APPLICANT: Umbeck, Paul F.
APPLICANT: Umbeck, Paul F.
APPLICANT: Umbeck, Paul F.
TITLE OF INVENTION: GENETICALY ENGINEERED COTTON PLANTS
TITLE OF INVENTION: FOR ALTERED FIBER
CORRESPONDENCE ADDRESS: 18
CORRESPONDENCE ADDRESS: 18
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Quarles and Brady
STREET: P.O BOX 2113
STREET: P.O BOX 2113
STREET: P.O SOX 2113
COUNTRY: U.S.A.
ZIP: MISCONSIN
COUNTRY: U.S.A.
ZIP: S7701
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; DB 1; Length 913; 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             croanism: Gossypium hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STACE: 15 day old fiber cells
TISSUE TYPE: fiber cells
LIBRARY: CKFB15A1
LOOR: H6
US-08-530-797-2
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Best Local Similarity 58.9%; Pred. No. 0.21,
Matches 63; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: DISKLE - 3.50 INCH, B COMPUTER: Apple Macintosh SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA: APPLICATION NATA: APPLICATION NUMBER: US/08/530,797 FILING DATE: 20.5EP-1995 CLASSIFICATION: 800 PRIOR APPLICATION NUMBER: US/08/530,243 FILING DATE: 21.NOV-90 APPLICATION NUMBER: US/07/53,243 FILING DATE: 04.0CT-88 ATTORNEY/AGENT INFORMATION: NAME: NICHOLAS J. Seay REGISTRATION NUMBER: 27,386 RESISTRATION NUMBER: 27,386 REGISTRATION NUMBER: 27,386 REGISTRATION NUMBER: 27,386 REGISTRATION NUMBER: 27,386 REFERENCE/DOCKET NUMBER: 1122990245 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08298829
patent No. 5620882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 913 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-298-829-3
US-08-530-797-2
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-298-687A-25
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                                                                                    ENGINEERED COTTON PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 ACCICCAGCITCICCACCICCICCACTCCICCACCAGCITCICAC 426
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                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,335
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Patent No. 5495070
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANDARISM: Gossypium hirsutum
STRAIN: Coker 312
DEVELOPMENTAL STAGE: 15 day old fiber cells
TISSUE TYPE: fiber cells
IMMEDIATE SOURCE:
LIBRARY: CKFB15A1
CLONF.
      APPLICANT: JOHN, Maliyakal E.
APPLICANT: Umbeck, Paul F.
APPLICANT: Umbeck, Paul F.
APPLICANT: Brill, Winston J.
TITLE OF INVENTION: GENETICALY ENGINEERE
TITLE OF INVENTION: FOR ALTERED FIBER
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles and Brady
STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
CITY: MADISON
STATE: MISCONSIN
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,797
FILING DATE: APPLICATION NUMBER: 05/253,243
FILING DATE: 04-CCT-88
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
REGISTRATION NUMBER: 27,386
REFENCE/DOCKET NUMBER: 1122990245
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 913 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
GENERAL INFORMATION:
APPLICANT: John,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CLONE: H6
US-08-787-335-2
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198 TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGCC 257
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Patent No. 5521078
GENERAL INFORMATION:
APPLICANT: JOHN, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36.6; DB 1;
Pred. No. 0.27;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady STREET: P.O. Box 2113, First Wisconsin Plaza CITY: Madison STATE: Wisconsin COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Nicholas J. Seay, Quarles & Brady STREET: P.O. Box 2113, First Wisconsin Plaza
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Best Local Similarity 58.9%; Pred. No. 0.27
Matches 63; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,970A
FILING DATE: 19920518
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: 04-0CT-1988
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 27,386
TELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION INFORMATION INFORMAT
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STRAIN: Sea Island
IMMEDIATE SOURCE:
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HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1984 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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CLONE: SIH6
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COMPUTER: IBM PC compatible
SOFFWARTER MICROSOFT WORD
SOFFWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,829
FILING DATE: 19-0CT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/885,970
FILING DATE: 18-MAY-1992
PRIOR APPLICATION NUMBER: US 07/617,239
FILING DATE: 18-MAY-1992
PRIOR APPLICATION NUMBER: US 07/53,243
FILING DATE: US 07/253,243
FILING DATE: US 07/253,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Gossypium barbadense
STRAIN: Sea Island
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.9%;
Matches 63; Conservative
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; CLONE: SIH6
US-08-298-829-25
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US-09-130-114-1
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Pred. No. 0.27;
0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AGCCAAGGCAGCCGCGCTCCTGCCGGGGGGGATCGGCTGAGCCGC 304
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Sequence 25, Application US/08298829

Patent No. 5620882

GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: GENETICALLY ENGINEERING COTTON
TITLE OF INVENTION: PLANTS FOR ALTERED FIBER
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STRET: P.O. Box 2113, First Wisconsin Plaza
CTTY: Madison
STATE: Wisconsin
COUNTRY: USA
                                                                                              COMPUTER READABLE FUAM:

MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/298,687A
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/617,239
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/253,243
FILING DATE: Q4-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
TELECHONE: (608) 283-2478
INFORMATION FOR SEQ ID NO: 25:
SEQUIENCE CHARACTERISTICS:
LENGTH: 1985 base pairs
TELENGTH: 1985 base pairs
TELENGTH: 1985 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossypium barbadense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%;
58.9%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 58.99
Matches 63; Conservative
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STRAIN: Sea Island
IMMEDIATE SOURCE:
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; CLONE: SIH6
US-08-298-687A-25
             Wisconsin
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198 TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGCC 257
                                                                                                                                                                                            Sequence 1, Application US/09130114

Patent No. 5976807

GENERAL INFORMATION:
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Evkaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: Evkaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: Evkaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
TITLE OF INVENTION: 1909 408-06

CURRENT FILING DATE: 1998 -08-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 5452
Score 36.6; DB 1; Length 1985;
Pred. No. 0.27;
0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                        629 Accrecascricaccrecacerecacaceaecascricases 675
                                                                                                                                                                                                                                                           258 AGCCAAGGCAGCCGCGCTGCCGCGGCGCGATCGGCTGAGCCGC 304
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Search completed: April 2, 2000, 22:08:40 Job time: 11896 sec

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                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/07884811

Patent No. 5316921

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION:

APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION:

STREET: 460 POINT SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 POINT San Bruno Blvd

CITY: South San Francisco

STREET: 460 POINT San Bruno Blvd

CITY: South San Francisco

STREET: 460 POINT San Bruno Blvd

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IMP PC compatible

OPERATING SYSTEM: PCOSS/MS-DOS

SOFTWARE: Datin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 15.00 MARE:

FILING DATE: 1992018

FILING DATE: 19920518

FILING DATE: 19920518

FILING DATE: 19920518

TELESTRATION NUMBER: 755.1

TELECOMMUTICATION INFORMATION:

MARE: DESGET ALS/225-3981

TELERA: 415/225-3981

TELERA: 110/311-7168

SEQUENCE CHARACTERISTICS:

LENGTH: 10596 bases
                                                                                                                      198 TCATACCAATAGGACTICTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCAGGGCC 257
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6.1%; Score 36; DB 4; Length 5452; 60.0%; Pred. No. 0.54; tive 0; Mismatches 40; Indels
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                   Best Local Similarity 60.09
Matches 60; Conservative
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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1 CAGGTACAGCGTAACGGCTT......AAACGAGCTCCGTGGCGATA 594
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                           4538634 segs, 1887831982 residues
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Listing first 45 summaries
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AL053013 Drosophil AL098770 Drosophil

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Description

SUMMARIES

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Genoscope.

Direct Submission

Burett Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EGCP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department o Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence SP6 end of BAC BACN9111 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 CCAGCCAAGGCAGCCGCGCCTCCTGCCGCGGCGCGATCGGCTGAGCCGCACGTGGGGAGC 315
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1036)
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                                                                                                                                                                                                                                                                                                                     172
                                                                                                                                                                                                                        /organism="Drosophila me/db_xref="taxon:7227"
/clone_lib="RPCI - 98"
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Direct Submission

Submitted (O2-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkely brosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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           d'Etudé du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03J03 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                        94 CGGTCCTCCCGCAGGGAAGAACAGCAGCCAGGCCAAAAAAACATCGGTAGTGGCGACGGCG 153
                                                                                                                                                                                                                                                                                                                                                                154 AAACCGGGGTGTGTGTCCTCGGGCACTGACGGGGGGGGTAGCAGTCGATACGACT 213
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
BAC) was made by Alain Billaud at CEPH (Centre
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/organism="Drosophila melanogaster"
/plasmid="peloabAC11"
/plasmid="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03H11"
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Pred. No. 2.5;
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Similarity 23.6%;
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of lowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7e1: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.ulowa.edu
Oligo-df track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLML (info@image.llnl.gov). IMAGE
ID=1776747 The following repetitive elements were found in this
cDNA sequence: 15-121, >(CAG)n#Simple_repeat 61-179,
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UI-R-A0-bd-d-010-011.s1 UI-R-A0 Rattus norvegicus cDNA clone
UI-R-A0-bd-d-01-0-01 3' similar to gb|AA42729|AA422729 vd29b05.s1
Knowles Solter mouse 2 cell Mus musculus cDNA clone 793913 5', mRNA
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library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbelobACII.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 447)
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/organism="Drosophila melanogaster"
/plasmid="pbelobaCl1"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03J03"
/note="end: T7"
/note="end: T7"
/note="end: T7"
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La Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP prosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of cancer Genetics at the Roswell Park Cancer Cantertute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                                                                                                                                     /strain="Sprague_Dawiey"
/db.zref="texon:10116"
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/lab_host="DH10B (Life Technologies)"
/note="vector: p7730-pac (Pharmacia) with a modified
/note="vector: p7730-pac (Individually tagged normalized
libraries constructed from rat placenta, adult lung,
brain, liver, kidney, heart, spleen, ovary, and muscle.
The tag is a string of 35 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 CGGTAGTGGCGACGGCGAAACCGGGGTGTGTGTCTCCGGGCACTGACGCGGCGAGTAGCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 GTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGC 256
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 CAGCCAAGGCAGCCGCGCGCTCCTGCCGCGGCGCGATCGGCTGAGCCGCACGTGG 310
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1 Similarity 52.3%; Pred. No. 7.6;
91; Conservative 0; Mismatches 83;
                                                                                                                 /organism="Rattus norvegicus"
                                                                      Location/Qualifiers
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>(CGG)n#Simple_repeat
Seq primer: M13 Forward
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU057847 550 bp mRNA EST 29-APR-1999
AU057847 Oryza sativa mature leaf Nipponbare Oryza sativa CDNA
Clone S21840_22, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     160 GGGTGTGTGTCCTCGGGCACTGACGCGGCGAGTAGCAGTCATACCAATACGACTTCTGCC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 SSGSGYGKGCSSGSGBSCSCCSSCSSSSSCSCCBCCCCCSCSSTCCSSSBSSSKCSSTS 614
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                                                                                                                                                                                                                                                          511 others
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                                                                                                                1. .925
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RRC1-98"
/clone="BACR19D16"
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230 CCCCTGCATCACCCCCTGTTTCAGCGCCAGCCAAGGCAGCCGCGCCCTCCTGCCGCGGCGC 289
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al Similarity 50.5%;
94; Conservative (
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                                                                                290 GATCGGCTG 298
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AA413349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F.rubripes GSS sequence, clone 021G08aAl, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                     309 ACGGGTTCAGCCGGCTCAACGTCCGCAACCACGAGCCCTTCTTCCCCCTCGACGACGACG 250
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                                                        1. .550
/organism-"Oryza sativa"
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/clone="$21840_22"
/clone_11b="Oryza sativa mature leaf Nipponbare"
/tissue_type="mature leaf"
a 120 c 201 g 103 t 2 others
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/db_xref="taxon:31033"
/clone_11b="cosmid 021G08"
/clone="021G08aA1"
54 c 43 g 50 t
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54.3%; Pred. No. 20;
                                                                                                                                                                                                                                         6.8%; Score 40.2; 53.5%; Pred. No. 13
             Email: tsasaki@abr.affrc.go.jp
PROJECT ='RGP'.
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Location/Qualifiers
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Fax: 0298-38-7468
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Matches 70; Conserv
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AgEST00022 Anopheles gambiae adult pSport cDNA Anopheles gambiae
258 ccecceccecarcacarccecrccargargargargargeccecceccecceccecceccec 317
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                                                                                                                                                                                                                                                                                                                                                                        African malaria mosquito.
Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Mepazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Culicoidea; Culicidae; Anopheles.

( Cases I to 623)
Cornel, A.J. Kumar V., Mukabayire, O., Salazar Rafferty, C.,
Petrarca, V., Coluzzi, M. and Collins, F. H.
A comprehensive physical map of the malaria vector Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Anopheles gambiae adult psport cDNA"
/sex="Male and Female"
/note="Site_l: Sall; Site_2: Not!; See: Salazar,
al. Insect Molecular Biology (1994), 3:1-13."
196 c 221 g 52 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Centers for Disease Control and Prevention
MS F-22, 4770 Buford Hwy, Chamblee, GA 30341
Tral: 770 488 7469
Fax: 770 488 7469
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: czs7@cdc.gov
Mapping location: 23C in 2L chromosome
Seq primer: M13 Reverse
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AA413349
AA413349.1 GI:2071903
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Location/Qualifiers
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/db_xref="taxon:7165"
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human.
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                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa; Catarrhini; Hominidae; Homo.

1. [bases 1 to 472]

8. Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K. Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. Washu-NcI human EST Project

1. Upublished (1997)

1. Upublished (1997)

1. Unu 12, 1998 Hils sequence version replaced gi:3246732.

1. Contect: Wilson RK

1. Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

1. Tais 286 1800

1. Fax: 314 286 1800

1. Fax: 314 286 1800

1. Fax: 314 286 1800

2. Fax: 314 286 1800

2. Fax: 314 286 1800

3. Fax: 314 286 1800

4. High quality sequence stop: 433.

1. Location/Qualifiers

1. Location/Qualifiers
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5'-GAGAGAGACTCGAGTTTTTTTTTTTTTTT3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length errichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area Science Park, Trieste, Italy).
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                                        AW162815 472 bp mRNA EST 09-NOV-1999 au87e07.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783268 5' similar to contains element TAR1 repetitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:2783268"
/clone_lib="Schneider fetal brain 00004"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
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/db_xref="taxon:9606"
                                                                                                           lement ;, mRNA sequence.
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AW162815.1 GI:6301848
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RESULT
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E 1 (bases 1 to 472)

S Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kriman, D., Kuchan, B., Kalaman, D., Kuchan, T., Lady, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, T., Lady, M., Le, N., Lennon, G., Marra, M., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washbor. CI human EST Project

Unpublished (1997)

On Jun 22, 1998 this sequence version replaced g1:3247266.

Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Fax: 314 286 1810
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/dev_stage="5 months post-conception"
/lab_host="DH10B"
/note="Corgan: brain; Vector: pBluescript SK (Stratagene);
Site_1: Sst1; Site_2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40RP from Glaco
High quality sequence stop: 417.
Location/Qualifiers
AW163342 472 bp mRNA EST 09-NOV-1599 au94a08.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783894 5' similar to contains TAR1.b2 TAR1 repetitive element; mRNA sequence.
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                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="InMGE:2783894"
/clone_lib="Schneider fetal brain 00004"
/sex="male"
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                                                                                                                          AW163342
AW163342.1 GI:6302375
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Matches 63; Conserva
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Submitted (22-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 CGGTAGTGGCGAACGGCGAAACCGGGGTGTGTGTCTCGGGGCACTGACGCGGCGGCGAGTAGCA 196
                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/organism="Drosophila melanogaster"
/plasmid="paelobacil"
/db_xref="taxon:7227"
/clone_lib="DrosBaC"
/clone="BACN37L08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 6.5%; Score 38.4; DB 80;
1 Similarity 15.1%; Pred. No. 40;
67; Conservative 182; Mismatches 195;
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                                                     Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Sequence is the complete cDNA Insert. hit genomic sequence AL024484
Plate: 39 row: B column: 12
High quality sequence stops: 513.
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/clone_lib="LP Drosophila melanogaster larval-early pupal
                                                                              AI260212 571 bp mRNA EST 17-NOV-1998 1003924. Sprime Le Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster CDNA clone. Lp03924 5prime similar to X61945: ng3 FBgn0010295 PID:9296042 SWISS-PROT:P40140, mRNA
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL108460.1 GI:55287FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
/note="Organ: whole body: Vector: pOT2; Site_1: EcoR1;
Shote="Organ: whole body: Vector poT2; Site_1: EcoR1;
ligated into pOT2. Plasmid cDNA library.
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                                                                                                                                                                                                                                                                                                               Truit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Meoptera; Endopterygota; Diptera; Erachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 571)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HIMI Drosophila EST Project
Unpublished (1997)
Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley, CSSS BERKeley, CSSS 128, Berkeley, CSSS 128, Berkeley, CSSS 128, SSSS 128, SSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38.4; DB 44; Length 571; Pred. No. 34; 0; Mismatches 56; Indels 0;

    .571
    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"

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AIZ60212.1 GI:3867737
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Best Local Similarity 56.2%;
Matches 72; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 c
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                     RESULT 11
AI260212/c
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
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Indels

Length 1101;

359 others

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257 CAGCCAAGCCAGCCGCGCCTCCTGCCGCGCGCATCGGCTGAGCCGCACGTGGGGAGCA 316
                                                                                                                                                                                                                                                                                                                                                                         377 GCACTGGAGCGCCGGCCACGACGACGTCTACGGCGGTGACGTCCACGACTACCGCCCCGC 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 ATAGTGGTGCCAGCGCGCCTCGTCTCCCACAGCCGCGGAAAACCAACAGGAGAAGAAA 556
698 ACMAADCGGCCAKMACCSSSSASSGSSCASTSSSASRGGMVSSCACSGSGGASACGA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI114969 538 bp mRNA EST 02-SEP-1998 ui41b06.yl Sugano mouse embryo mewa Mus musculus cDNA clone
                                                                    197 GTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGC
                                                                                                                                                                                                    317 AGATCATTGCTAATCTAGTGAATCAGCTGGGGATTAATGTCACCCAAAGGAGCGTCGTCA
                                                                                                                                                                                                                                                                                                       437 AGCGAACAAGTCCATACGGGCACAATGGCCGACCTGTGACGGCTGGATTGGTGGCAGCTA
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AI131654.1 GI:3601670
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AI131654
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                                                                                                                                                                                                                                 Mus musculus
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Best Local Simi
Matches 82;
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    14
                                                                    DEFINITION
                                                                                                                                                                                                                               ORGANISM
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  RESULT 1
AI131654
LOCUS
                                                                                                                                                                                KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pME185-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG): 1st strand cDNA was primed with an oligo(dT) primer [ArTGTGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTGTGCTGTAAAAGCTGG and 3' end primer CTTGTGCTGTAAAAGCTGG and 3' end primer
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 538)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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IMAGE:1884947 5' similar to TR:014633 014633 SKIN-SPECIFIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 ACATCGGTAGTGGCGACGGCGAAACCGGGGTGTGTGTCTCCGGGCACTGACGCGGCGAGT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 AGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 ACCACTGCTGCTGCCACACCACTGCTGCCACCGCTGCTGCTGCCACAACTGCTGCC 380
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                                                                                                                                                                                                                                                                                                                 Waterston, R.
The MasNu-HHMI Mouse EST Project
Unpublished (1996)
On Jan 17, 1998 this sequence version replaced gi:1900380.
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:1884947"
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH108"
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Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 GCGCCAGCCAAGGCAGCCGCGCCTCCTGCCGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 490.
Location/Qualifiers
1. 538
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                                                                 AI114969.1 GI:3515293
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Best Local Similarity 52.9%;
Matches 82; Conservative (
                         ;, mRNA sequence.
                                                                                                                                      Mus musculus
                                                                                                                house mouse.
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ORIGIN
                                                                                                                                      ORGANISM
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AUTHORS
                                               ACCESSION
                                                                                    KEYWORDS
SOURCE
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/clone_ine_Traxon:10097
/clone_ine_Traxon:10097
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="bill0B"
/lab_host="bill0B"
/note="vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); lst strand cDNA was primed
with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
CURCTGGCTTAAAGCTGCG and 3' end primer
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                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Mammalia;
Butheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.
1 (bases 1 to 814)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
AII31654 814 bp mRNA EST 14-SEP-1998 ui41b06.x1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:1884947 3' similar to TR:014633 014633 SKIN-SPECIFIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Un Sep 12, 1996 this sequence version replaced gi:1402281.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
H444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 41;
0; Mismatches
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/organism="Mus musculus"
/strain="C57BL"
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High quality sequence stop: 375.
Location/Qualifiers
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                    AA756319 436 bp mRNA EST 21-JAN-1998 vv40h01.rl Soares 2NDMT Mus musculus cDNA clone IMAGE:1224913 5/ similar to TR:Q99331 Q99331 NEUTROPHIL PROTEIN; mRNA sequence. AA756319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (196)
On Jan 19, 1998 this sequence version replaced gi:2045795.
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Pred. No. 38;
0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 404.
253 GCGCCAGCCAAGGCAGCCGCGCCTCCTGCCGCGGC 287
                      543 GCCACAGCAACTGCTGCCACCGCTGCTGCCACAGC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1224913"
/clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                    AA756319.1 GI:2803517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.4%;
Best Local Similarity 55.2%;
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .436
                                                                                                                                                                                                                                                           house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
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                                                                                             RESULT 15
AA756319/c
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ORIGIN
                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                  VERSION
KEYWORDS
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225 TGCATCCCCTGCATCACCCCCTGTTTCAGCGCCAGCCAAGGCAGCCGCGCCTCCTGCCGC 284

285 GGCGCGATCGGCTG 298

86 TGCTGCCACTGCTG 73

2, 2000, 19:13:11 Search completed: April Job time: 1623 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April Run on:

US-08-988-242-1\_COPY\_1232\_1825 Perfect score:

... AAACGAGCTCCGTGGCGATA 594 1 CAGGIACAGCGIAACGGCIT Seguence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 segs, 125096042 residues Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

N\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	anosoma cruz	1 cDNA. New	virus gB g	l protein	SCA2 gene CAG repe	ine rich	Cotton fiber-speci	Cotton fibre-speci	n fibre cell	Cotton fibre speci	ibre s	fibre-	0	Cotton H6 gene and	of the M3/6	the M3/6	Genomic Eimeria te	t stabi	¥	las	Plasmid pCisEBON f	Plasmid pCisEBON f	Nucleotide sequenc	rty	of th	Eimeria tenella sp	adenosine	ರ	æ	3	pinocerebellar a	Spinocerebellar at	Spinocerebellar at	Spinocerebellar at
SUMMAKIES	<b>.</b>	D	T27310	V18480	T16480	T42903	V17226	V30271	T07199	T13034	T30253	T62610	T70041	T13030	T30250	T70036	T86757	T86758	Q03322	V55830	V55831	V21683	Q51731	T40348	x15650	V43674	N92576	T93593						Q84834		
	é	DB	Н	-	-	H	_	-	-	-	H		Н	Н	-	Н	Н	Н	Н	Н	ч	Н	-	Н	Н	Н		Н	~	-1	П	г	٦	Н	7	П
		Length	3402	79	94	11	203	203	913	913	913	913	91	98	98	1985	41	45	633	795	79	960	029	10596	059	0	80	108	95	46	41	3376	168	171	195	234
æ	Query		99.5											•	٠	•			•	•	•	•	•			•	•	•		•		•			•	•
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P. americanus skin EST clone DN740. N	DNA encoding B. la Brevibacterium lac	B. lactofermentum	Brevibacterium lac	Loricrin gene. Con	EST clone CP328. N	Human secreted pro	Choline oxidase ge	Choline oxidase ge
T75505 V90494	T49282 T84788	V15788	V40257	051557	V89532	V80740	T42859	T75000
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35 35	34.8 34.8	34.8	34.8	34.8	34.6	34.6	34.6	34.6
35 36	37	39	40	41	42	43	44	45
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## ALIGNMENTS

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PF 12-AUG-1994; 010132.

PR 12-AUG-1994; FR-010132.

PR 12-AUG-1994; FR-010132.

PI JOJIVET M. Lesenechal M. Paranhos-Baccala G;

JOJIVET M. Lesenechal M. Paranhos-Baccala G;

JOJIVET M. Lesenechal M. Paranhos-Baccala G;

WPI 96-190287/20.

BR PSEDER, R91615.

PR WOW NUCLPLC, acid_encoding Trypanosoma cruzi epimastigotic antigen -

PT useful for diagnosis, monitoring and therapy of Chagas disease

Claim 1; Page 24-25. S5pp; French.

This is the nuclectide sequence encoding a novel isolated antigenic

protein from Trypanosoma cruzi epimastigotes, designated Prc100t.

The clone TC50 was isolated from a T cruzi genomic expression library in

Lambda gtll, using a mixture of sera from patients with Chagas disease.

Clone TC50 contained an 594 bp insert corresp. to nucleotides 1232-1825

Cof this sequence. The TC50 sequence was subsequently used to probe a

Southern blot of restriction enzyme digested T cruzi DNA and also screen

a lambda gtll library to isolate a 1041 bp EcoRI fragment corresp. to

conclectides 1403-2443 of Prc100t. Primers (T27311-5) were synthesised

conclides from T cruzi epimastigotes. The protein or antibodies raised

constituted from T cruzi epimastigotes. The protein or antibodies raised

contection i.e. Chagas disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                            26-Nov-1996 (first entry)
Trypanosoma cruzi epimastigotic PTc100t antigen gene.
Antigen; Trypanosoma cruzi, epimastigote; serum; Chagas disease; probe; Primer; PCR; polymerase chain reaction; amplification; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1232 CAGGTACAGCGTAACGGCTTTTGCTTCAATCGTACAGCCGACGGTAGCTGCGTCCTGGCT 1291
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266. 3013
/*teg al.
/product- PTCi00t epimastogotic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.5%; Score 590.8; DB 1; Best Local Similarity 99.7%; Pred. No. 1.2e-140; Matches 592; Conservative 0; Mismatches 2;
                                       standard; cDNA; 3402 BP.
                                                                                                                                                             Trypanosoma cruzi
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RESULT
T27310
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                                                                                                                                                                                                                                                                                                                                                                                         Corticotroph; pituitary; BOP1; tumour suppressor; constitutive; inducible; alzheimer's disease; nuclear transcription factor; apoptosis; cell cycle; neuronal disorder; ss.
                   1471
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                                                                                                                                           540
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                                                                                                                                                                             480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the BOPI CDNA isolated from the mouse corticotroph pituitary tumour cell line Atr-20 cDNA ilbrary. The protein encoded by the BOPI CDNA displays a tumour suppressing activity when it was constitutively and inducibly expressed in tumour cells. The BOPI cDNA and the protein it encodes are claimed to be useful in the preparation of therapeutic compositions, useful for treating, preventing or delaying the recurrence of a tumour or neuronal disorders, e.g. genetic diseases or acquired degenerative encephalopathies such as Alzheimer's disease. The BOPI protein is also claimed to be able to induce apoptosis resulting in inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to act as nuclear transcription factor 783 C; 714 G; 626 T;
       CCCCCTGTTTCAGCGCCAGCCAGCCGCGCGCCTCCTGCCGCGGCGGCGATCGGCTGAG
                                                                                                                                                                                        GGATTGGTGGCAGCTAATAGTGGTGCCAGCGCGGCGTCGTCTCCCACAGCCGCGGGGAAA
                                                                                    CCGCACGTGGGGAGCAAGATCATTGCTAATCTAGTGAATCAGCTGGGGATTAATGTCACC
                                                                                                                               CAAAGGAGCGTCGCCACTGGAGCGCCGGCCACGACGAGGTCTACGGCGGTGACGTCC
                                                                                                                                                                            ACGACTACCGCCCCCCAGCGAACAAGTCCATACGGGCACAATGGCCGACCTGTGACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              formation, to induce Gl
                                                                                                                                                                                                                                                                              1772 CCAACAGGAGAAGAGGCCTCCGCGGCATGTGAAACGAGCTCCGTGGCGATA 1825
                                                                                                                                                                                                                                                                    CCAACAGGAGAAAAAGGCCTCCGCGGCATGTGAAACGAGCTCCGTGGCGATA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated tumour suppressor gene - useful for developing for use in diagnosis and treatment of tumour(s) or neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CNRS ) CENT NAT RECH SCI.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour cell growth, to suppress tumour est of the cell cycle and to act as nuc uence 2790 BP; 667 A; 783 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "BOP1 protein"
                                                                                                                                                                                                                                                                                                                                               V18480 standard; cDNA to mRNA; 2790 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
542. .2545
                                                                                                                                                                                                                                                                                                                                                                    18-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO981342,
02-APR-1998,
22-SEP-1997; E05198,
17-1996; US-718661,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Journot L, Spengler D; WPI; 98-230701/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W48760
                                                                                                                                                                                                                                                                                                                                                                              BOP1 cDNA.
Corticotroph;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder(s)
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Length 2790;

DB 1;

Score 39.2; DB Pred. No. 0.31;

6.68; 54.18;

Query Match Best Local Similarity

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                                                                                                             137 CGGTAGTGGCGACGGCGAACCGGGGTGTGTCCTCGGGCACTGACGCGGCGAGTAGCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of herpes B virus by PCR amplification of sample DNA - to detect a specific herpes simian monkey B virus DNA segment.

Disclosure, Column 23-30, 22pp; English.

This sequence encodes the herpes simian monkey SA8 virus gB glycoprotein. Such sequences have been used to develop synthetic DNA primers which have homologous sequences of conserved regions which flank a divergent region of the gB glycoprotein gene. In addition, proteins such as the gB glycoprotein have potential use in the development of serological immunoassays, one approach is to synthesize peptides which, based on the properties of the predicted protein sequence, are likely to be immunologically active. Such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides can be used as substrate antigens in immunoassays to detect serum antibodies which recognize this specific peptide sequence. Synthetic peptides may also be used to produce antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific regions of the gB glycoprotein which are unique to one virus. These can then be used to develop virus-specific immunoassays for differentiation of SAB virus from other primate alpha-herpes viruses and for identification of antibodies directed against SAB virus in primate serum samples. 983 G; 395 T;
                                                                                                                                                                         197 GTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGACGGGGAGGGAAGAAGGAGGGGGGGGGGCCGCGAGGCCGCATCCCGGGGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 ATCTAGTGAATCAGCTGGGGATTAATGTCACCCAAAGGAGCGTCGTCAGCACTGGAGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SA8 virus gB glycoprotein coding sequence.
Herpes simian monkey SA8 virus gB glycoprotein; immunoassay;
diagnosis; herpes B virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38.2; DB 1; Length 2:
Pred. No. 0.57;
0; Mismatches 123; Indels
Indels
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   68;
   Mismatches
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Black D, Eberle R, Hilliard J, Scini
WPI; 96-105220/11.
                                                                                                                                                                                                                                                                                                                                                   2234 CAGATGCAGCTACCACAGCTGCTGCCGC 2261
                                                                                                                                                                                                                                                                                         257 CAGCCAAGGCAGCCGCGCTCCTGCCGC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simian monkey SA8 virus.
Key Location/Qualifiers
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Best Local Similarity 47.7
Matches 112; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993; 042747.
01-APR-1993; US-042747.
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number of CAG repeat units
Example 1; Page 12; 23pp; Japanese.
                                                                                                                                        99
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                                                                                                                                                                                                                                                                                                                     and for detecting cancer claim 17. This sequence was used in claim 17, page 48-54; 77pp; Japanese.

This sequence encodes the protein TSP-1. This sequence was used in conjunction with a DNA molecule with gene expression regulation activity, in a plasmid for regulation of gene expression, and treatment of viral infection pref. human T-cell leukaemia and HIV. The plasmid also encodes a protein which is used as an antivirus agent, and also in a method for detecting cancer. The DNA molecule and protein have potential uses in denetherapy, and the plasmid may also have potential use in the treatment of TSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCA2 gene CAG repeat unit fragment.
SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                               DNA molecule with gene expression regulation activity - for use in e.g. treatment of human T-cell leukaemia and HIV, as antivirus agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - by PCR and determining
                                                                                 16-JUN-1997 (first entry)
TRP-1 protein coding sequence.
gene expression; regulation; plasmid; viral infection;
human T-cell leukaemia; HIV; antivirus agent; detection; cancer;
gene therapy; TSP; ds.
        389 CGCCCACGACGAGGTCTACGGCGGTGACGTCCACGACTACCGCCCCGCAGCGAAC 443
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 36.8; DB 1; Length 3776; 69.4%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Indels
                                                                                                                                                                                                                                                                               Sakaguchi
                                                                                                                                                                                                                                                                                Saiga A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing spinocerebellar ataxis type II
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                Orita S,
                                                                                                                                                                                                     /product= TRP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V17226 standard; DNA; 203 BP. V17226;
                                                                                                                                                                              /*tag= a
                                                                                                                                                                                                                                                         27-APR-1995; JP-104299.
(SHIO) SHIONOGI & CO LTD.
Igarashi H, Okumura K, O
WPI; 96-455367/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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29-JAN-1998.
18-JUL-1996; J01999.
18-JUL-1996; WO-J01999.
(SRLS-) SRL INC.
Sanpei K, Tsuji S;
                                                                                                                                                                                                                                                24-MAR-1995; JP-066559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1415 AGCCCCAGAGCC 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 ATCGGCTGAGCC 302
                                                                                                                                                                                                                                     19-MAR-1996; J00719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                   P-PSDB; W06136
                                                                                                                                                                                                                WO9630522-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 5
                                                            RESULT
T42903
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Example 1; Page 22; 38pp; Japanese.

Example 1; Page 22; 38pp; Japanese.

This represents a sequence encoding glutamine rich repeat region which can be found in spinocerebellar ataxia type 2 (SCA2) patients. The specification provides a gene sequence causative of the neurodegenerative of sequence from Gln-166 to patients this number is increased to 35-100. Peptides encoded by nucleic acid fragments (DNA or RNA) containing sequences from the SCA2 associated complex antibodes recognising the peptides and antisense nucleic acids hybridising with the nucleic acid fragments can be used for the investigation and diagnosis of SCA2. They can also be used for the creatment of SCA2 by antisense therapy or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocarebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocarebellar ataxis type II.

Sequence 203 BP; 68 A; 70 C; 62 G; 3 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 GCGGCGAGTAGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-0CT-1998 (first entry)
Glutamine rich region encoding sequence found in SCA2 patients.
Spinocerebellar ataxia type 2; SCA2; gene therapy; antisense therapy;
CAG repeat; neurodegenerative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 GCGGCGAGTAGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanpei K, Tsuji S;
WPI; 98-272215/724
WPI; 98-272215/724
WPI acid fragments associated with spinocerebellar ataxia type
- contain increased number of CAG repeat region compared to normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 CCTGTTTCAGCGCCAGCCAAGGCAGCCGCGCCTCCTGCCGCGGCGCGCGATCGGCTG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 203;
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57.4%; Pred. No. 0.79;
Live 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V30271 standard; DNA; 203
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30-OCT-1997; J03946.
30-OCT-1996; JP-304059.
(SRLS-) SRL INC.
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Matches 66; Conserv
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WO9818920-A1.
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Gossypium hi
US5521078-A.
                                                                                                                                                                                                                                                                                                                                               16-DEC-1996
                                                                                                                                                                                                                                                                                                                                      T30253;
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                                                                                                                                                                                                                                                                                                                                                          Cotton
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T30253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 TCCACCCAGITCICCICCICCICCACCACCACCIGCITCICCICCICCICCACCCC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGCC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                 T07199;
10-MAY-1996 (first entry)
Cotton fiber-specific H6 protein gene.
H6 gene; promoter; cotton; transgenic plant; fiber; immobilisation;
enzyme; pesticide degradation; parathion hydrolase; extensin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 713034;
27-MAY-1996 (first entry)
27-MAY-1996 (first entry)
Cotton fibre: promoter: transgenic plant; crop improvement; ds. Gossypium hirsutum strain Coker 312.
Key
72. 716
                                                                                                                                                                                                                                             Preport of immobilised enzymes in cotton fibre - esp. pesticide-degrading enzymes e.g. parathion hydrolase bisclosure; Column 31-34; 37pp; English by the cotton Hig gene (707198) encodes an extensin-like protein (R86913) that is an integral part of the secondary cell wall of cotton. The portions of the gene encoding the N-terminal or transmembrane regions of the protein may be utilised in the construction of gene fusions used to anchor (i.e. immobilise) foreign proteins in the fibers of transgenic cotton plants. Fusions of H6 and a foreign protein should be localised within the secondary walls of the fiber. The immobilised proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.6; DB 1; Length 913; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                       249 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
                                                                                                                                                                                                                                                                                                                                                                  e.g. enzymes or antibodies, have industrial, medical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AGCCAAGGCAGCCGCGCCTCCTGCCGCGCGCGCGATCGGCTGAGCCGC 304
                                                                                                                                                                                                                                                                                                                                                                                      155 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      313 C;
                                                                    Gossypium hirsutum strain Coker 312
Key Location/Qualifiers
cds 72. .716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T13034 standard; cDNA; 913 BP
                                                                                                                                                                                                                                                                                                                                                                                     196 A;
       T07199 standard; DNA; 913 BP
                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%;
58.9%;
                                                                                                  /*tag= a
72..147
/*tag= b
148..713
/*tag= c
                                                                                                                                                                        19-DEC-1991; 812233.
19-DEC-1991; US-812233.
23-MAR-1994; US-217337.
(CETU ) AGRACETUS INC.
Barton KA, Maliyakal J;
WPI; 96-039513/04.
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 58.9
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-1996,
04-0CT-1988; 253243,
04-0CT-1988; US-253243,
21-NOV-1990; US-617239,
18-MAY-1992; US-885970,
                                                                                                                                                                                                                                                                                                                                                                           environmental applns.
Sequence 913 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CETU ) AGRACETUS INC.
John M;
WPI; 96-139095/14.
                                                                                                             signal_peptide
                                                                                                                                                                                                                                       P-PSDB; R86913
                                                                                                                                  mat_peptide
                                                                                                                                                                12-DEC-1995
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This cDNA clone contains an insert of 500 bp which hybridised with a 950 bp RNA. It is expressed in fibres but not in root, flower, leaf or ovules. The sequence suggests a single open reading frame extending from bases 71-710. This sequence has been deposited with ATCC at accession on 67810.

The promoters isolated from the fibre cell-specific clones can be used to generate transgenic cotton plants and lines producing fibres having altered quantity and quality.

Sequence 913 BP; 196 A; 313 C; 155 G; 249 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolation of fibre-specific cotton promoter sequences - using selected DNA probes to screen genomic DNA fragments, for production of cotton fibres with improved characteristics

Examples: Column 25-28; 46pp; English:
Cotton fibre cell-specific promoter sequences were isolated by differential screening of a cotton plant cDNA library. Of 4788 clones from a 10 day cell library screened with leaf cDNAs, 800 clones not present in the leaf were isolated. These were screened with CDNAs from ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR analysis was then used to remove cross-hybridising clones. This resulted in the isolation of 18 cDNA clones specifically expressed in cotton fibre cells (130242-4 and 730253-67). These cDNAs were then used to screen for homologous genomic sequences (130245-53 and 130268) in order to obtain
New isolated fibre-specific promoters - used for introducing altered fibre-specific characteristics into plants, partic. cotton. Example 3; Column 25-28; 48pp; English.

Cotton fibre-specific cDNA chone H6 (T13034) (ATCC 67810) was cotton fibre-specific cDNA chone H6 (T13034) (ATCC 67810) was isolated from a cDNA library of cotton var. Coker 312 15-day-old boll cells by a subtractive hybridization procedure. It hybridizes to a developmentally regulated RNA of 950 bases that is not detected in leaf, flower, ovule or root. The putative protein product is proline-rich and clearly distinct from previously known plant cell wall proteins. H6 and other fibre-specific cDNA clones (see T1303-T13050) were used to screen cotton genomic libraries, leading to the isolation of genomic clones (see T13025-53) contg. sequences capable of promoting gene expression in fibre cells. Sequence 913 BP; 196 A; 313 C; 155 G; 249 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cotton fibre; promoter; differential screening; leaf; ovule; root; flower; PCR; polymerase chain reaction; homology; transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCAGCGCC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996 (first entry)
fibre cell-specific cDNA clone CKFB15Al-H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36.6; DB; Pred. No. 1.1; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%;
58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T30253 standard; DNA; 913 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2
Best Local Similarity 58.9
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAY-1996.
04-0CT-1988; 253243.
04-0CT-1988; US-253243.
21-NOV-1990; US-617239.
18-MAY-1992; US-885970.
19-0CT-1994; US-298687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hirsutum
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Sequence.
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                                                                                                                                                                                                                                                                                                           DNA molecule with gene expression regulation activity - for use in e.g. treatment of human T-cell leukaemia and HIV, as antivirus agent and for detecting cancer.

Claim 17: Page 48-54; 77pp; Japanese.

This sequence encodes the protein TSP-1. This sequence was used in conjunction with a DNA molecule with gene expression regulation activity, in a plasmid for regulation of gene expression, and treatment of viral infection pref. human T-cell leukaemia and HIV. The plasmid also encodes a protein which is used as an antivirus agent, and also in a method for detecting cancer. The DNA molecule and protein have potential uses in gene therapy, and the plasmid may also have potential use in the treatment of TSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V17226;
29-JUN-1998 (first entry)
SCA2 gene CAG repeat unit fragment.
SCA2 gene; spinocerebellar ataxis type II; CAG repeat; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 CCCTGCATCACCCCCTGTTTCAGCGCCAGCCAAGGCAGCCGCGCGCCTCCTGCCGCGGGGGCGCG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by PCR and determining
                                                                                   16-JUN-1997 (first entry)
TRP-1 protein coding sequence.
gene expression; regulation; plasmid; viral infection;
human T-cell leukaemia; HIV; antivirus agent; detection; cancer;
gene therapy; TSP; ds.
         389 CGGCCACGACGAGGTCTACGGCGGTGACGTCCACGACTACCGCCCCGCAGCGAAC 443
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 36.8; DB 1; Length 3776; 69.4%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                   Sakaguchi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1183 G;
                                                                                                                                                                                                                                                                                 Igarashi H, Okumura K, Orita S, Saiga A,
WPI; 96-455367/45.
P-PSDB; W06136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing spinocerebellar ataxis type II
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1177 C;
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                139. .2205
/*tag= a
/product= TRP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                764 A;
                                                                                 T42903 standard; DNA; 3776 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16/c
V17226 standard; DNA; 203 BP.
                                                                                                                                                                                                                                    19-MAR-1996; J00719.
24-MAR-1995; JP-066559.
27-APR-1995; JP-104299.
(SHIO ) SHIONGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1998.
18-JUL-1996; J01999.
18-JUL-1996; WO-J01999.
(SRLS-) SRL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 ATCGGCTGAGCC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sanpei K, Tsuji S;
WPI; 98-120796/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                м09803679-А1.
                                                                                                                                                                                                                  WO9630522-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T42903
                                                                                    g
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Example 1; Page 22; 38pp; Japanese.

This represents a sequence encoding glutamine rich repeat region which
can be found in spinocerebellar ataxia type 2 (SCA2) patients. The
specification provides a gene sequence causative of the neurodegenerative
disease SCA2, having a tri-nucleotide (CAG) repeat region which in the
expression product produces a polyglutamine sequence from Gln-166 to
CG for-188. In the normal gene there are 15-25 CAG repeats but in SCA2
patients this number is increased to 35-100. Peptides encoded by nucleic
cald fragments (DNA or RNA) containing sequences from the SCA2 associated
CG gene, antibodies recognising the peptides and antisense nucleic acids
hybridising with the nucleic acid fragments can be used for the
chreatment of SCA2 by antisense therapy or gene therapy.
Sequence 203 BP; 68 A; 70 C; 62 G; 3 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
number of CAG repeat units
Example 1; Page 12; 23pp; Japanese.
This sequence represents a fragment of the SCA2 gene. It can be used in the method of the invention for diagnosing spinocerebellar ataxis type II, by performing PCR on the test DNA using two primers hybridising to parts of the SCA2 gene sequence, and determining the number of CAG repeats in the amplified products. The method provides an easy means for the diagnosis of spinocerebellar ataxis type II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glutamine rich region encoding sequence found in SCA2 patients. Spinocerebellar ataxia type 2; SCA2; gene therapy; antisense therapy; CAG repeat; neurodegenerative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 GCGGCGAGTAGCAGTCCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 GCGGCGAGTAGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 GCCCAGAGITICCGTGAIGCIGCIGCIGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI: 98-272215/24.
Nucleic acid fragments associated with spinocerebellar ataxia type - contain increased number of CAG repeat region compared to normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.6; DB 1; Length 203; Pred. No. 0.79; 0; Mismatches 49; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 6.2%; Score 36.6; DB 1;
Best Local Similarity 57.4%; Pred. No. 0.79;
Matches 66; Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 6.2%;
Best Local Similarity 57.4%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V30271/c
ID V30271 standard; DNA; 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1998.
30-0CT-1997; J03946.
30-0CT-1996; JP-304059.
(SRLS.) SRL INC.
Sanpei K, Tsuji S;
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WO9818920-A1.
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for introducing

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WPI; 96-267794/27
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16-DEC-1996
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             John M;
                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                 130253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCAGCGCC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                          10-MAY-1996 (first entry)
Cotton fiber-specific H6 protein gene.
H6 gene; promoter; cotton; transgenic plant; fiber; immobilisation; enzyme; pesticide degradation; parathion hydrolase; extensin; ds. Gossypium hirsutum strain Coker 312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.7.0.7.
27.0.7.
27.0.7.
Cotton fibre-specific cDNA clone H6.
Cotton; fibre; promoter; transgenic plant; crop improvement; ds.
Gossypium hirsutum strain Coker 312.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                          Preport of immobilised enzymes in cotton fibre - esp. pesticide-degrading enzymes e.g. parathion hydrolase Disclosure; Column 31-34; 37pp; English, properticide-degrading enzymes e.g. parathion hydrolase Disclosure; Column 31-34; 37pp; English; English The cotton fig ene (100198) encodes an extensin-like protein (R86913) that is an integral part of the secondary cell wall of cotton. The portions of the gene encoding the N-terminal or transmembrane regions of the protein may be utilised in the construction of gene fusions used to anchor (i.e. immobilise) foreign proteins in the fibers of transgenic cotton plants. Fusions of H6 and a foreign protein should be localised within the secondary walls of the fiber. The immobilised proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 913;
                                                                                                                                                                                                                                                                                                                                                                                                             249 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                    e.g. enzýmes or antibodies, have industrial, medical and
environmental appins.
Sequence 913 BP; 196 A; 313 C; 155 G; 249 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AGCCAAGGCAGCCGCGCCTCCTGCCGCGCGCGCATCGGCTGAGCCGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 ACCTCCAGCTTCTCCACCTCCTGCACTCCTCCACCAGCTTCTCCCAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.6;
Pred. No. 1.
                                                                                     Location/Qualifiers 72. .716
                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%;
58.9%;
        T07199 standard; DNA; 913 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T13034 standard; cDNA; 913
                                                                                                        /*tag= a
72. .147
                                                                                                                             /*tag= b
148. .713
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2
Best Local Similarity 58.9
Matches 63; Conservative
                                                                                                                                                                                                                    (CETU ) AGRACETUS INC.
Barton KA, Maliyakal J;
WPI; 96-039513/04.
P-PSDB; R86913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1990; US-617239.
18-MAY-1992; US-885970.
(CETU ) AGRACETUS INC.
John M;
WPI; 96-139095/14.
                                                                                                                                                    /*tag=
                                                                                                                                                                                                         23-MAR-1994; US-217327.
                                                                                                                                                                                   19-DEC-1991; 812233.
19-DEC-1991; US-812233.
                                                                                                                    signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-1996.
04-OCT-1988; 2
04-OCT-1988; U
                                                                                                                                                                           -DEC-1995.
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                                                                                                                                                              US5474925-A
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Examples; Column 25-28; 46pp; English.
Cotton fibre cell-specific promoter sequences were isolated by differential screening of a cotton plant cDNA library. Of 4788 clones from a 10 day cell library screened with leaf cDNAs, 800 clones not present in the leaf were isolated. These were screened with cDNAs from ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR analysis was then used to remove cross-hybridising clones. This resulted in the isolation of 18 cDNA clones specifically expressed in cotton fibre cells (T30242-4 and T30253-67). These cDNAs were then used to screen for honologous genomic sequences (T30245-53 and T30268) in order to obtain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell-specific clones can be used to lines producing fibres having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cotton fibre cell-specific cDNA clone CKFB15A1-H6.

Cotton fibre; promoter; differential screening; leaf; ovule; root; filower; PCR; polymerase chain reaction; homology; transgenic plant; ds. US5521078-A.
US5521078-A.
US5521078-A.
US53243.
U-CCT-1988; US-253243.
U-CCT-1988; US-853243.
US-007-1999; US-858970.
US-007-1994; US-858970.
US-007-1994; US-2986970.
CETU ) AGRACETUS INC.
Altered fibre-specific characteristics into plants, partic. cotton. Example 3; Column 25-28; 48pp; English.

Cotton fibre-specific conA clone H6 (T13034) (Arcc 67810) was soluted from a cDNA clone H6 (T13034) (Arcc 67810) was soluted from a cDNA library of cotton var. Coker 312 15-day-old boll cells by a subtractive hybridization procedure. It hybridizes to a developmentally regulated RNA of 950 bases that is not detected in leaf, flower, ovule or root. The putative protein product is proline-rich and clearly distinct from previously known plant cell wall proteins. H6 and other fibre-specific cDNA clones (see T13033-T13050) were used to screen cotton genomic libraries, leading to the isolation of genomic clones (see T13025-32 and T13052-53) contg. sequences capable of promoting gene expression in fibre cells. Sequence 913 Bp; 196 A; 313 C; 155 G; 249 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCCTGTTTCAGCGCC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This cDNA clone contains an insert of 500 bp which hybridised with a 950 bp RNA. It is expressed in fibres but not in root, flower leaf ovules. The sequence suggests a single open reading frame extending from bases 71-710. This sequence has been deposited with ATCC at accession no. 67810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.2%; Score 36.6; DB 1; Length 913; 58.9%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 ACCICCAGCITCICCACCICCACCICCACCAGCITCICCAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AGCCAAGGCAGCCGCGCGTCTGCCGCGCGCGCGATCGGCTGAGCCGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The promoters isolated from the fibre generate transgenic cotton plants and altered quantity and quality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the corresp, promoter sequences.
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Matches 63; Conservative
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RESULT T62610

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obtain genomic clones containing bibre-specific promoters. Claimed DNA constructs comprise a truncated promoter sequence (from one of 170031-38) constructs comprise a truncated promoter sequence (from one of 170031-38) that promotes preferential gene expression in plant fibre cells, a protein coding sequence not naturally associated with the promoter sequence and a 3' termination sequence. The DNA constructs are useful for expressing foreign genes in fibre-producing plants, esp. to produce transgenic cotton plants with varied cotton fibre characteristics and quality. The present sequence comprises H6 CDNA isolated from clone (KFB15A1-H6 (CK = Coker; FB15 = 15 day old bolls). This sequence has a single protein coding region between nucleotides 71 and 710. This gives a proline rich peptide of 214 amino acids. A total of 5 amino acids (Ala, Pro, Leu, Ser and Val) make up 74.3% of the protein. The sequence comprises the clone repeats of X-Y-Pro-Pro-Pro repeat units where X and Y are Ser, Ala or Thr. The H6 CDNA clone was deposited with ATCC accession number 67810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 ICATACCAATACGACTICIGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGCC 257
                                                                                                                                                                                                                                                                                                                   DNA constructs contg. truncated promoter sequence for fibre-specific gene expression in cotton plants
Example 3: Column 27-28: 48pp. English
T70040-57 are cotton fibre-specific cDNA clones which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.30.0.7.
27.AMY-1996 (first entry)
Cotton fibre-specific H6 gene and promoter.
Cotton; fibre; promoter; transgenic plant; crop improvement; ds.
Gossypium barbadense strain Sea Island.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%; Score 36.6; DB 1; Length 913; 58.9%; Pred. No. 1.1;
/note= "contains putative open reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/*note= "the CDS includes a 583 bp intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AGCCAAGGCAGCCGCGCCTCCTGCCGCGCGCGATCGCCTGAGCCGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 ACCICCAGCITCICCACCICCIGCCACTCCTCCACCAGCITCICCAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.1;
0; Mismatches
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1548. .1984
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T13030 standard; DNA; 1984 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 A;
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/*tag= b
321. .1547
/*tag= c
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.320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 58.9 63; Conservative
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US-617239.
US-885970.
                                                                                                                  US-253243.
US-617239.
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                                                                                                                                                21-NOV-1990; US-617239.
18-MAY-1992; US-885970.
19-OCT-1994; US-298829.
                                                                                                                                                                                                                                    (CETU ) AGRACETUS INC
                                                                                             253243
                                                                                                                                                                                                                                                                                        WPI; 97-235185/21
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21-NOV-1990; U
18-MAY-1992; U
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04-OCT-1988;
                                                                                       04-OCT-1988;
04-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5495070-A.
                                 US5620882-A
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Best Local S
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T13030
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162609-24 are cotton fibre-specific cDNA clones which can be used to Idéntify genomic clones. This clone, CKFBISA1-Me, is developmentally regulated. The E6 RNA was found to be developmentally regulated. (CR = Coker; FB = Fibre; 10, 15 or 23 = age in days of fibre cells; Al and the last character and number stand for clone identity). The fibre-specific genes were identified by differential cDNA library screenings. Coding sequences from these isolated genes are used in sense or antisense orientation to alter the fibre characteristics, e.g. strength, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TCATACCAATACGACTTCTGCGGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGCC 257
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                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding sequence or E6 anti-sense sequence, produces fibre of altered
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Cotton fibre specific cDNA clone CKFB15A1-H6.
cotton; fibre-specific; strength; transgenic plant; anthesis; developmentally regulated; E6; H6; antisense; sense; ss. Gossypium hirsutum strain Coker 312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 913;
         Length 913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-Aug-1997 (first entry)
Cotton fibre specific cDNA clone H6.
Cotton; E6; fibre; promoter; transgenic plant; truncated;
deterologous gene expression; ds.
Gossypium hirsutum strain Coker 312.
Key
71. .710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                  44; Indels
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            DB 1;
         Score 36.6; Di
Pred. No. 1.1;
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36.6;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 T62610 standard; cDNA to mRNA; 913 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic fibre-producing plants.
Sequence 913 BP; 196 A; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) AGRACETUS.
Brill WJ, John ME, Umbeck PF;
WPI: 97-108326/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.2%;
Similarity 58.9%;
63; Conservative
            6.2%;
58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-1988; 253243.
04-OCT-1988; US-253243.
21-NOV-1990; US-1739.
18-OCT-1993; US-138814.
20-SEP-1995; US-530797.
                                                                        Conservative
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Best Local Similarity
            Query Match
Best Local Similarity
Matches 63; Conserv
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(CETU ) AGRACETUS INC

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Matches

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H6 CDNA)
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Cotton fibre cell-specific promoter sequences were isolated by differential screening of a cotton plant cDNA library. Of 4788 clones differential screening of a cotton plant cDNA library. Of 4788 clones from a 10 day cell library screened with leaf cDNAs, 800 clones not present in the leaf were isolated. These were screened with cDNAs from ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR analysis was then used to remove cross-hybridising clones. This resulted in the isolation of 18 cDNA clones specifically expressed in cotton fibre
                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1996 (first entry)
Cotton fibre clone SKSIE6-H6-RI-derived promoter contg. sequence.
Cotton fibre; promoter; differential screening; leaf; ovule; root;
flower; PCR; polymerase chain reaction; homology; transgenic plant; ds.
                                                                                                                                                                                                                                                                            TCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCTGTTTCAGCGCC 257
                                                                                                                                                                                                                                                                                              Gaps
                                   altered fibre-specific characteristics into plants, partic. Cotton. Claim 1; Column 59-62; 48pp; English.

The cotton var. Sea Island HG gene and promoter (T13030) were identified in genomic clone EMBL-S1-H6-4 isolated by Screening a genomic library prepd. in lambda EMBL with cotton fibre-specific construction of vectors used for the introduction of altered fibre-specific promoters can be utilised in the specific characteristics into plants, partic. cotton. They can be used to modulate the synthesis of fibre proteins or to introduce non-fibre proteins into fibre in a tissue-specific manner. Sequence 1984 BP; 555 A; 470 C; 281 G; 668 T;
                                                                                                                                                                                                                                                         ö
                         New isolated fibre-specific promoters - used for introducing
                                                                                                                                                                                                                               DB 1; Length 1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "contains promoter sequence (claimed)"
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                               258 AGCCAAGGCAGCCGCGCTCCTGCCGCGCGCGCATCGGCTGAGCCGC 304
                                                                                                                                                                                                                                                                                                                                             ACCTCCAGCTTCTCCACCTCCTGCCACTCCTCCAGCTTCTCCCAC 675
                                                                                                                                                                                                                                                       44;
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hoote= "contains a 583 bp intron"
1548. 1984
/*tag= d
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/note= "5' non-coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-coding sequence"
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                              Score 36.6;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        T30250 standard; DNA; 1985 BP.
                                                                                                                                                                                                                           6.2%;
ilarity 58.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1547
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19-OCT-1994; US-298687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gossypium barbadense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253243.
John M;
WPI; 96-139095/14.
                                                                                                                                                                                                                                        Similarity
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04-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                     63;
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                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
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Matches
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T30250
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Claim 1; Column 61-64; 48pp. English.

TO0031-38 are genomic DNA clones containing cotton fibre-specific promoters. Claimed DNA constructs comprise a truncated promoter sequence (from one of T70031-38) that promotes preferential gene expression in plant fibre cells, a protein coding sequence not naturally associated with the promoter sequence and a 3' termination sequence. The DNA with the promoter sequence and a 3' termination sequence. The DNA plants, esp. to produce transgenic cotton plants with varied cotton fibre characteristics and quality. The present sequence comprises a fragment of plants, esp. (an EcoRI fragment isolated from pSKSIH6-4 which hybridises to
                                                                                                                                                                                      used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
cells (T30242-4 and T30253-67). These CDNAs were then used to screen for homologous genomic sequences (T30245-53 and T30268) in order to obtain the corresp. promoter sequences.

This genomic clone is derived from the 1.9 kb Sall-EcoRI fragment of the sub-clone designated SKSIE6-6RI. This forms part of the genomic clone designated as EMBL-SI-H6-4 which contains a 13 kb Mbol insert.

The promoters isolated from the fibre cell-specific clones can be used to generate transgenic octton plants and lines producing fibres having
                                                                                                                                                                                                                                                                                                                                                                                                                                              198 TCATACCAATACGACTTCTGCCGCTGCATCCCCTGCATCACCCCCTGTTTCAGCGCC 257
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                                                                                                                                                                                                                                                                   668 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-Aug-1997 (first entry)
Cotton H6 gene and fibre-specific promoter from clone SIH6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      668 T;
                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cotton; E6; fibre; promoter; transgenic plant; truncated; heterologous gene expression; ds. Gossypium barbadense strain Sea Island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 AGCCAAGGCAGCCGCGCCTCCTGCCGCGGCGCGATCGGCTGAGCCGC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629 ACCTCCAGCTTCTCCACCTCCTGCCACTCCTCCACCAGCTTCTCCAC 675
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                                                                                                                                                                                                                                                             282 G;
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                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                             Score 36.6; D
Pred. No. 1.3;
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58.9%; Pred. No. 1.
                                                                                                                                                                                                                                                          470 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 C;
                                                                                                                                                                                                                                                       565 À;
                                                                                                                                                                                                                     altered quantity and quality. Sequence 1985 BP; 565 A;
                                                                                                                                                                                                                                                                                                                                    6.2%;
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                                                                                                                                                                                                                                                                                                                                                                                             63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-617239.
US-885970.
US-298829.
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04-OCT-1988; US-2532
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Matches 63; Conserv
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19-0CT-1994;
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                                                                                                                                                                                                                                                                                                                                          Query Match
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Claim 1: Fig 1: 51pp: English.

Claim 1: Fig 1: 51pp: English.

This cDNA is said to encode a murine phosphatase designated M3/6 (see also T86758). M3/6 is a suspected dual specificity Threonine-Tyrosine phosphatase, capable of inactivating mitogen activated protein (MAP)

Ckinase. The M3/6 protein product shows high homology to the cdc25 PTP of yeast at residues 29-49 and 117-136. The gene also contains a complex criplet distal to the catalytic domain which is translated into the protein. This domain comprises a tun of 4 serine residues which in turn comprises a run of 4 serine residues which in turn is followed by a further run comprising 23 serine residues which in turn comprises a can of is followed by a further run comprising 23 serine residues which in turn comprises a can of is serine residues which in turn comprises a can of its followed by a further run comprising 23 serine residues which is meakes the phosphatase gene a candidate for a human disease caused by repeat expansion or mutation. M3/6 is expressed highly in the brain and compressed highly in the brain and confidences, if mutated, for various neurodegenerative or proliferative diseases, and may therefore be used for the diagnosis of such diseases, confinitions to treat these diseases.

Sequence 2415 BP; 491 A; 764 C; 678 G; 465 T;
                                                                                                                                       cDNA of the M3/6 gene. "I", murine; prosine; Tyrosine; murine; phosphatase; M3/6; dual specificity; Threonine; Tyrosine; inactivate, mitogen activated protein kinase; MAP-K; cdc25 PTP; yeast; trinucleotide repeat; repeat expansion; neurodegenerative; proliferative; diagnosis; tumour; lung; brain; chromosomal deletion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-154253/14.
Murine mitogen activated protein (MAP) kinase phosphatase M3/6 - is a suspected dual specificity Thr-Tyr phosphatase, useful for diagnosing and treating neuro-degenerative or proliferative diseases
                                                    T86757 standard; cDNA; 2415 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                           (MEDI-) MEDICAL RES COUNCIL.
Davies KE, Theodosiou A;
                                                                                                            15-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                        20-FEB-1997.
05-AUG-1996; G01906.
04-AUG-1995; GB-016059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97-154253/14.
                                                                                                                                                                                                                                                                                   Mus sp.
WO9706245-Al.
RESULT 15
T86757/c
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186 GGCGAGTAGCAGTCATACCAATACGACTTCTGCCGCTGCTGCATCCCCTGCATCACCCCC 245 Gaps ö 6.1%; Score 36.4; DB 1; Length 2415; 59.8%; Pred. No. 1.6; 41; Indels 1809 TGTTGCTGCTGCTGCTGCCGCCGCCGCCGCCGCCGC 1768 246 IGTITCAGCGCCAGCCAAGGCAGCCGCGCCTCCTGCCGCGGC 287 0; Mismatches 61; Conservative Best\_Local Similarity Matches 61; Conserv g ò ò

Query Match

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Search completed: April 2, 2000, 21:55:09 Job time: 11056 sec

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